

65		70		75		80
Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln	85		90		95	
Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg Leu	100		105		110	
Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys	115		120		125	
Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg	130		135		140	
Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp	145		150		155	160
Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro	165		170		175	
Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp	180		185		190	
Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu	195		200		205	
Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg	210		215		220	
Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp	225		230		235	240
Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu	245		250		255	
Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly	260		265		270	
Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu	275		280		285	
Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro	290		295		300	
Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro	305		310		315	320

Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Glu Gly Arg Val  
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 His Arg Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala  
 340 345 350  
 Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly  
 355 360 365  
 Val Ala Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Phe Thr Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 Phe Gln Asn Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430  
 Gln Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
 435 440 445  
 Arg Gly Val Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu  
 450 455 460  
 Leu Glu Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala  
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 Phe Asp Glu Leu Gly Leu Thr Pro Val Gly Arg Thr Gln Lys Thr Gly  
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 Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His  
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 Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys  
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 Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly  
 545 550 555 560  
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
 565 570 575



Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
 580 585 590

Gly Gln Arg Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu  
 595 600 605

Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
 610 615 620

Ser Gly Asp Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile  
 625 630 635 640

His Thr Glu Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val  
 645 650 655

Asp Pro Lys Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr  
 675 680 685

Lys Glu Ala Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
 690 695 700

Val Arg Ala Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly  
 705 710 715 720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala  
 725 730 735

Ser Arg Val Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
 740 745 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val  
 755 760 765

Lys Leu Phe Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln  
 770 775 780

Val His Asn Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu  
 785 790 795 800

Ala Lys Ala Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp  
 805 810 815

Val Pro Leu Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala

820

825

830

Lys Gln Asp  
835

&lt;210&gt; 342

&lt;211&gt; 38

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic

&lt;400&gt; 342

tggcggcggc ctcgggcggc cgcgtccacc gggcaaca

38

&lt;210&gt; 343

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic

&lt;400&gt; 343

cttctctcat ccgcaaaaac agcc

24

&lt;210&gt; 344

&lt;211&gt; 38

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic

&lt;400&gt; 344

tggccgccgc ctggggcggc cgcgtttacc gggcggag

38

&lt;210&gt; 345

<211> 2505

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 345

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ccggtgcaga tggctctacgg cttcgccccg agcctcctca aggccttgaa ggaggacgga      180
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gcctacaagg cgggcccgggc cccacccccg gaggacttcc cccgccagct cgccttggtc      300
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gccgttttgg cctgcggga ggggggtggc ctggacccca cggacgacct cctcctggtg     1140
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ctctcctttg agctggagaa ggagatggag cgcctggagg gggaggtctt ccgtttggcc     1440
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<210> 346

<211> 835

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 346

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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Tyr	Ala	Leu
			20					25					30		

Ser	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Met	Val	Tyr	Gly	Phe
		35					40					45			

Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
 65 70 75 80  
 Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg Leu  
 100 105 110  
 Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg  
 130 135 140  
 Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp  
 145 150 155 160  
 Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro  
 165 170 175  
 Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp  
 180 185 190  
 Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu  
 195 200 205  
 Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp  
 225 230 235 240  
 Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu  
 245 250 255  
 Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro  
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val  
 325 330 335

His Arg Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala  
 340 345 350

Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly  
 355 360 365

Val Ala Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Phe Thr Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

Phe Gln Asn Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430

Gln Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
 435 440 445

Arg Gly Val Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu  
 450 455 460

Leu Glu Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala  
 465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495

Phe Asp Glu Leu Gly Leu Thr Pro Val Gly Arg Thr Gln Lys Thr Gly  
 500 505 510

Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His  
 515 520 525

Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys  
 530 535 540

Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly

545		550		555		560									
Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu
				565					570					575	
Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu
			580					585					590		
Gly	Gln	Arg	Ile	Arg	Lys	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Leu	Leu
		595					600					605			
Leu	Ala	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu
	610					615					620				
Ser	Gly	Asp	Glu	Asn	Leu	Lys	Arg	Val	Phe	Arg	Glu	Gly	Lys	Asp	Ile
625					630					635					640
His	Thr	Glu	Thr	Ala	Ala	Trp	Met	Phe	Gly	Leu	Asp	Pro	Ala	Leu	Val
				645					650					655	
Asp	Pro	Lys	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu
			660					665					670		
Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Gly	Ile	Asp	Tyr
	675						680					685			
Lys	Glu	Ala	Glu	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys
	690					695					700				
Val	Arg	Ala	Trp	Ile	Glu	Arg	Thr	Leu	Glu	Glu	Gly	Arg	Thr	Arg	Gly
705					710					715					720
Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Ala
				725					730					735	
Ser	Arg	Val	Arg	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn
			740					745					750		
Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Ile	Ala	Met	Val
		755					760					765			
Lys	Leu	Phe	Pro	Arg	Leu	Lys	Pro	Leu	Gly	Ala	His	Leu	Leu	Leu	Gln
	770					775					780				
Val	His	Asn	Glu	Leu	Val	Leu	Glu	Val	Pro	Glu	Asp	Arg	Ala	Glu	Glu
785					790					795					800

Ala Lys Ala Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp  
805 810 815

Val Pro Leu Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala  
820 825 830

Lys Gln Asp  
835

<210> 347

<211> 2496

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 347

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caggcggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg      180
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<210> 348

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 348

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val  
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Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu  
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys  
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val  
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr  
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val  
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala  
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu  
130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr  
145 150 155 160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser  
165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile  
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg  
195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys  
210 215 220

Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys  
225 230 235 240

Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val  
 245 250 255  
 Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe  
 260 265 270  
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285  
 Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300  
 Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
 305 310 315 320  
 Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val Tyr Arg Ala Glu  
 325 330 335  
 Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu Leu  
 340 345 350  
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu Ala  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala Leu  
 405 410 415  
 Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu  
 420 425 430  
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val Glu  
 450 455 460  
 Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg Leu Ala Gly His  
 465 470 475 480  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Ile Phe Asp  
 485 490 495

Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Gln Lys Thr Gly Lys Arg  
 500 505 510  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr  
 530 535 540  
 Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu  
 545 550 555 560  
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590  
 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val Val  
 595 600 605  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His Thr  
 625 630 635 640  
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Ser  
 645 650 655  
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 660 665 670  
 Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu Glu  
 675 680 685  
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg  
 690 695 700  
 Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr Val  
 705 710 715 720  
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg  
 725 730 735  
 Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro

740	745	750
Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu		
755	760	765
Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His		
770	775	780
Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val Ala		
785	790	795
Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val Pro		
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Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Ala		
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<210> 349

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 349

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caggcggtgg tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcctacgag	240
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<211> 2505

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

<400> 350

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<210> 351

<211> 835

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 351

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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Tyr Ala Leu
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Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe

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Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu
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Glu	Ala	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Gly	Thr	Leu	Ala	Lys
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Lys	Ala	Glu	Arg	Glu	Gly	Met	Glu	Val	Arg	Ile	Leu	Thr	Gly	Asp	Arg
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Gly	Thr	Leu	Val	Thr	Pro	Lys	Asp	Val	Gln	Glu	Lys	Tyr	Gly	Val	Pro
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Pro	Glu	Arg	Trp	Val	Asp	Phe	Arg	Ala	Leu	Thr	Gly	Asp	Arg	Ser	Asp
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Glu	Val	Asp	Phe	Lys	Ala	Leu	Arg	Arg	Arg	Thr	Pro	Asp	Leu	Glu	Gly
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Leu	Arg	Ala	Phe	Leu	Glu	Glu	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu
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Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro  
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Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val  
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His Arg Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala  
340 345 350  
Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly  
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Val Ala Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu  
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Asp Pro Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
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Glu Phe Thr Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu  
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Phe Gln Asn Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr  
420 425 430  
Gln Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
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Arg Gly Val Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu  
450 455 460  
Leu Glu Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala  
465 470 475 480  
Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
485 490 495  
Phe Asp Glu Leu Gly Leu Thr Pro Val Gly Arg Thr Gln Lys Thr Gly  
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Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His  
515 520 525  
Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys  
530 535 540

Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly  
545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
580 585 590

Gly Gln Arg Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu  
595 600 605

Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
610 615 620

Ser Gly Asp Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile  
625 630 635 640

His Thr Glu Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val  
645 650 655

Asp Pro Lys Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr  
675 680 685

Lys Glu Ala Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
690 695 700

Val Arg Ala Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly  
705 710 715 720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala  
725 730 735

Ser Arg Val Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
740 745 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val  
755 760 765

Lys Leu Phe Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln  
770 775 780

Val His Asn Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu

785 790 795 800

Ala Lys Ala Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp  
805 810 815

Val Pro Leu Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala  
820 825 830

Lys Gln Asp  
835

<210> 352

<211> 2496

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 352

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<210> 353

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 353

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Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu  
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Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys  
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val  
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr  
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val  
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala  
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu  
130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr  
145 150 155 160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser  
165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile  
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg  
195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys  
210 215 220

Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys  
 225 230 235 240

Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val  
 245 250 255

Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe  
 260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285

Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300

Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
 305 310 315 320

Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val Tyr Arg Ala Glu  
 325 330 335

Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu Leu  
 340 345 350

Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu Ala  
 355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380

Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400

Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala Leu  
 405 410 415

Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu  
 420 425 430

Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445

Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val Glu  
 450 455 460

Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg Leu Ala Gly His  
 465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Ile Phe Asp  
485 490 495

Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Gln Lys Thr Gly Lys Arg  
500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
515 520 525

Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr  
530 535 540

Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu  
545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
580 585 590

Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val Val  
595 600 605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
610 615 620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His Thr  
625 630 635 640

Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Ser  
645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
660 665 670

Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu Glu  
675 680 685

Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg  
690 695 700

Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr Val  
705 710 715 720

Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg



725								730					735				
Val	Lys	Ser	Ile	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro		
			740				745						750				
Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu		
			755				760						765				
Phe	Pro	Arg	Leu	Gln	Glu	Leu	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His		
770						775						780					
Asn	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Gln	Ala	Glu	Glu	Val	Ala		
785						790						795		800			
Gln	Glu	Ala	Lys	Arg	Thr	Met	Glu	Glu	Val	Trp	Pro	Leu	Lys	Val	Pro		
			805						810						815		
Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Ala		
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<210>	354
<211>	42
<212>	DNA
<213>	Artificial Sequence

<220>  
<223> Synthetic

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<400> 354
ggcctcacc cgg tgaagcg gacgaagaag acgggcaagc gc
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42

<210>	355
<211>	42
<212>	DNA
<213>	Artificial Sequence

<220>  
<223> Synthetic

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<400> 355
gcgcttgccc gtcttcttcg tccgcttcac cggggtgagg cc
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42

<210> 356  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
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 <400> 356  
 ctcctcctcc aagtggccaa cgagctggtc ctg 33  
  
 <210> 357  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Synthetic  
 <400> 357  
 caggaccagc tcgttggcca cttggaggag gag 33  
  
 <210> 358  
 <211> 2505  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic  
 <400> 358  
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 ccggtgcaga tggctctacgg cttcgccccg agcctcctca aggccttgaa ggaggacgga 180  
 caggcggtgg tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacgag 240  
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 aagcggctgg tggaccttct gggcctggtc cgcctcgagg ccccggggta cgaggcggac 360

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ggggagaaga	ccgcccttcg	actcctcgca	gagtggggga	gcgtggaaaa	cctcctgaag	660
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gccaaagggcc tggtaagga ggtcatggag aacgcctacc ccctggacgt gcccctcgag 2460  
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<210> 359

<211> 835

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 359

Met Asn Ser Thr Pro Leu Phe Asp Leu Glu Glu Pro Pro Lys Arg Val  
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Tyr Ala Leu  
20 25 30

Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe  
35 40 45

Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg Leu  
100 105 110

Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys  
115 120 125

Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg  
130 135 140

Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp  
 145 150 155 160

Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro  
 165 170 175

Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp  
 180 185 190

Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu  
 195 200 205

Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg  
 210 215 220

Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp  
 225 230 235 240

Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu  
 245 250 255

Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly  
 260 265 270

Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285

Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro  
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val  
 325 330 335

His Arg Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala  
 340 345 350

Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly  
 355 360 365

Val Ala Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400





<223> Synthetic  
 <400> 360  
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 <211> 42  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic  
 <400> 361  
 gcgcttgccc gtcttcttcg tcttcttgat ggcgggaagc cc 42  
 <210> 362  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic  
 <400> 362  
 atgcttttgc aggtggccaa cgaactggtc ctc 33  
 <210> 363  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Synthetic  
 <400> 363  
 gaggaccagt tcgttggcca cctgcaaaag cat 33  
 <210> 364



<211> 2496

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 364

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caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg      180
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atggtggacc ttttgggcct ggagcgcctc gaggtgccgg gctttgaagc ggatgacgtc      360
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aagacggcgg ccaagctgat ccgggagtgg ggaagcctgg aaaaccttct taagcacctg      660
gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag      720
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gaggcggggg aaaggcgct gctttccgaa aggctttacg ccgccctcct gaagcggcct      1260
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cccgccatca agaagacgag gaagacgggc aagcgctcca ccagcgccgc cgttttggag 1560
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<210> 365

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 365

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Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1          5          10         15

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Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
          20          25         30

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```

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
          35          40         45

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Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val  
 50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr  
 65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
 85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val  
 100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala  
 115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu  
 130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr  
 145 150 155 160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser  
 165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile  
 180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg  
 195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys  
 210 215 220

Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys  
 225 230 235 240

Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val  
 245 250 255

Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe  
 260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285

Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300

Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
 305 310 315 320

Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val Tyr Arg Ala Glu  
 325 330 335

Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu Leu  
 340 345 350

Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu Ala  
 355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380

Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400

Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala Leu  
 405 410 415

Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu  
 420 425 430

Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445

Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val Glu  
 450 455 460

Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg Leu Ala Gly His  
 465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Ile Phe Asp  
 485 490 495

Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Arg Lys Thr Gly Lys Arg  
 500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525

Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr  
 530 535 540

Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu

545		550		555		560
His Thr Arg Phe	Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser	565		570		575
Ser Asp Pro Asn Leu Gln Asn Ile	Pro Val Arg Thr Pro Leu Gly Gln	580		585		590
Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val Val		595		600		605
Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly		610		615		620
Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His Thr		625		630		635
Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Ser		645		650		655
Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly		660		665		670
Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu Glu		675		680		685
Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg		690		695		700
Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr Val		705		710		715
Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg		725		730		735
Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro		740		745		750
Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu		755		760		765
Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His		770		775		780
Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val Ala		785		790		795
						800

Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val Pro  
805 810 815

Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Ala  
820 825 830

<210> 366

<211> 2505

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 366

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ccggtgcaga tgggtctacgg cttcgcccgg agcctcctca aggccttgaa ggaggacgga      180
caggcggtgg tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcctacgag      240
gcctacaagg cgggcccgggc cccacccccg gaggacttcc cccgccagct cgccttggtc      300
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gccgttttgg ccctgcggga ggggggtggc ctggaccca cggacgacct cctcctggtg     1140
gcctacctcc tggacctggc caacaccac cccgaggggg tggcccggcg ctacgggggg     1200

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cgccgggcgg ccaagacggt caacttcggc gtcctctacg ggatgtccgc ccacaggctc	2040
tcccaggagc tcggcataga ctacaaggag gcggaggcct ttattgagcg ctacttccag	2100
agcttcccca aggtgcgggc ctggatagaa aggaccctgg aggagggccg gacgcggggc	2160
tacgtggaga ccctgttcgg caggaggcgc tatgtgccc acctggcctc ccgggtccgc	2220
tcggtgcggg aggcggcgga gcggatggcc ttcaacatgc ccgtgcaggg caccgccgcc	2280
gacctgatga agatcgccat ggtcaagctc tccccaggc taaagcccct gggggccac	2340
ctcctctcc aagtggcaa cgagctggtc ctggaggctc ccgaggaccg ggccgaggag	2400
gccaaggccc tggatcaagga ggtcatggag aacgcctacc ccctggacgt gcccctcgag	2460
gtggagggtg gcgtgggtcg ggactggctg gaggcgaagc aggat	2505

<210> 367

<211> 835

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 367

Met Asn Ser Thr Pro Leu Phe Asp Leu Glu Glu Pro Pro Lys Arg Val

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Leu	Leu	Val	Asp	Gly	His	His	Leu
		20					25
							30
Ser	Leu	Thr	Thr	Ser	Arg	Gly	Glu
		35					40
							45
Ala	Arg	Ser	Leu	Leu	Lys	Ala	Leu
		50					55
							60
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro
							70
							75
Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro
							85
							90
Leu	Ala	Leu	Val	Lys	Arg	Leu	Val
			100				105
							110
Glu	Ala	Pro	Gly	Tyr	Glu	Ala	Asp
							115
							120
Lys	Ala	Glu	Arg	Glu	Gly	Met	Glu
							130
							135
Asp	Phe	Phe	Gln	Leu	Leu	Ser	Glu
							145
							150
Gly	Thr	Leu	Val	Thr	Pro	Lys	Asp
							165
							170
Pro	Glu	Arg	Trp	Val	Asp	Phe	Arg
							180
							185
Asn	Ile	Pro	Gly	Val	Ala	Gly	Ile
							195
							200
Leu	Ala	Glu	Trp	Gly	Ser	Val	Glu
							210
							215
Val	Lys	Pro	Asp	Ser	Leu	Arg	Arg
							225
							230
Leu	His	Leu	Ser	Leu	Asp	Leu	Ala
							245
							250
							255



Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly  
                   260                                  265                                  270

Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu  
                   275                                  280                                  285

Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro  
                   290                                  295                                  300

Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro  
                   305                                  310                                  315                                  320

Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val  
                                   325                                  330                                  335

His Arg Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala  
                                   340                                  345                                  350

Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly  
                   355                                  360                                  365

Val Ala Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu  
                   370                                  375                                  380

Asp Pro Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
                   385                                  390                                  395                                  400

Glu Phe Thr Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu  
                                   405                                  410                                  415

Phe Gln Asn Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr  
                                   420                                  425                                  430

Gln Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
                                   435                                  440                                  445

Arg Gly Val Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu  
                   450                                  455                                  460

Leu Glu Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala  
                   465                                  470                                  475                                  480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
                                   485                                  490                                  495

Phe Asp Glu Leu Gly Leu Thr Pro Val Lys Arg Thr Lys Lys Thr Gly  
                                   500                                  505                                  510

Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His  
 515 520 525  
 Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys  
 530 535 540  
 Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly  
 545 550 555 560  
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
 565 570 575  
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
 580 585 590  
 Gly Gln Arg Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu  
 595 600 605  
 Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
 610 615 620  
 Ser Gly Asp Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile  
 625 630 635 640  
 His Thr Glu Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val  
 645 650 655  
 Asp Pro Lys Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670  
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr  
 675 680 685  
 Lys Glu Ala Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
 690 695 700  
 Val Arg Ala Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly  
 705 710 715 720  
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala  
 725 730 735  
 Ser Arg Val Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
 740 745 750  
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val

755	760	765
Lys Leu Phe Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln		
770	775	780
Val Ala Asn Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu		
785	790	795
Ala Lys Ala Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp		
805	810	815
Val Pro Leu Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala		
820	825	830
Lys Gln Asp		
835		

<210> 368

<211> 2496

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 368	
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caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg	180
gtgatcgtgg tgtttgacgc caaggcccc tccttccgcc accagaccta cgaggcctac	240
aaggcggggc gggctccac ccccgaggac tttccccggc agcttgccct tatcaaggag	300
atggtggacc ttttgggctt taccgcctc gaggtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaaaag gaaggctacg aagtgcgcat cctcaccgcg	420
gaccgggacc tttaccagct tctttcggag cgaatctcca tccttcaccc ggaggggttac	480
ctgatcacc cggagtggct ttgggagaag tatgggctta agccttccca gtgggtggac	540
taccgggcct tggccgggga cccttccgac aacatccccg gcgtgaaggg catcggggag	600
aagacggcgg ccaagctgat ccgggagtgg ggaagcctgg aaaaccttct taagcacctg	660
gaacaggtga aacctgcctc cgtgcgggag aagatcctta gccacatgga ggacctcaag	720

ctatccctgg agctatcccc ggtgcacacg gacttgetcc ttcaggtgga cttcgccccg	780
cgccgggagc cggaccggga ggggcttaag gccttttttg agaggctgga gttcggaagc	840
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ccccccgagg gagccttcgt ggggtacgtt ctttcccgcc ccgagcccat gtgggcggag	960
cttaacgcct tggccgccgc ctggggcggc cgcgtttacc gggcgaggga tcccttgag	1020
gccttgccgg ggcttgggga ggtgaggggg cttttggcca aggacctggc ggtgctggcc	1080
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gaggcggggg aaagggcgct gctttccgaa aggctttacg ccgccctcct gaagcggtt	1260
aagggggagg agaggcttct ttggctttac gaggaggtgg aaaagcccct ttcgcggtc	1320
ctggcccaca tggaggccac gggggtagcg ttggatgtgg cctacttaaa ggccctttcc	1380
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cctttcaacc tgaactcccg ggaccagctg gaaagggta tctttgacga gcttgggctt	1500
cccgccatca agaagacgag gaagacgggc aagcgtcca ccagcgccgc cgttttggag	1560
gccttgccgg aggtcatcc catcgtggac cgcaccttc agtaccggga gctttccaag	1620
ctcaaggga cctacatcga tcccttgccct gccctggtcc accccaagac gaaccgcctc	1680
cacaccggt tcaaccagac ggccaccgcc acggggaggc ttagcagctc ggatccta	1740
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gaggaggggt ggaggctggt ggttttgac tacagccaga ttgagctcag ggtcctggcg	1860
cacctttccg gggacgagaa cctaaccgg gtcttcagg agggccagga catccacacc	1920
cagacggcca gctggatgtt cggcgtgcc ccagaggccg tggattccct gatgcgccg	1980
gcggccaaga ccatcaactt cggcgtcctc tacggcatgt ccgcccaccg gctttcggga	2040
gagctggcca tcccctacga ggaggcggtg gccttcacg agcggtattt ccagagctac	2100
cccaagggtgc gggcctggat tgagaaaacc ctggcggaag gacgggaacg gggctatgtg	2160
gaaaccctct ttggccgccg gcgtacgtg ccgacttg cttcccgggt gaagagcatc	2220
cgggaggcag cggagcgcac ggccctcaac atgccggtcc aggggaccgc cgcggatttg	2280
atgaaactgg ccatggtgaa gctctttccc aggcttcagg agctgggggc caggatgctt	2340
ttgcagggtgc acaacgaact ggtcctcgag gctcccaagg agcaagcgga ggaagtcgcc	2400
caggaggcca agcggaccat ggaggaggtg tggccctga aggtgccctt ggagggtgga	2460
gtgggcatcg gggaggactg gctttccgcc aaggcc	2496

<210> 369

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 369

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val  
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Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu  
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys  
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val  
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr  
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val  
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala  
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu  
130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr  
145 150 155 160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser  
165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile  
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg  
 195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys  
 210 215 220

Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys  
 225 230 235 240

Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val  
 245 250 255

Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe  
 260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285

Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300

Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
 305 310 315 320

Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val Tyr Arg Ala Glu  
 325 330 335

Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu Leu  
 340 345 350

Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu Ala  
 355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380

Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400

Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala Leu  
 405 410 415

Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu  
 420 425 430

Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445

Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val Glu  
450 455 460

Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg Leu Ala Gly His  
465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Ile Phe Asp  
485 490 495

Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Arg Lys Thr Gly Lys Arg  
500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
515 520 525

Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr  
530 535 540

Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu  
545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
580 585 590

Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val Val  
595 600 605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
610 615 620

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His Thr  
625 630 635 640

Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Ser  
645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
660 665 670

Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu Glu  
675 680 685

Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg





<220>  
 <223> Synthetic  
 <400> 371  
 ccctccgaca acctcaaggg ggtcaagggc atc 33

<210> 372  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic  
 <400> 372  
 gaggttgctg gaggggtc 18

<210> 373  
 <211> 2526  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic  
 <400> 373  
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 ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120  
 gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180  
 ggggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcctg ccacgaggcc 240  
 tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300  
 ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag 360  
 gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420  
 atcctcaccg ccgaccgga cctctaccaa ctctgtctcc accgcgtcgc cgtcctccac 480  
 cccgagggcc acctcatcac cccggagtgg ctttggggaga agtacggcct caggccggag 540  
 cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctcgc cggggtcaag 600  
 ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660

ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca cggacctccc cctggagggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcggca gcctcctcca cgagttcggc ctcttgaggg ccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc	960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca	1020
gacctcttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctctgtcccc gggacgacct catgctcctc	1140
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gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc	1260
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gagcttaggc ttccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
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acgggcccgc tccacaccgc cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
tccgacccca acctgcagaa catccccgtc cgcacccct tgggcccagag gatccgccgg	1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag	1920
gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc	1980
ctgatgcgcc gggcgggcaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac	2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac	2100
ttccaaagct tccccagggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag	2160
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgacct caacgcccgg	2220
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gccgcccacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg	2340
gcccgcacgc tcctccagggt cgccaacgag ctctcctcgg agggccccca agcgcgggcc	2400
gaggagggtg cggttttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc	2460
ctggagggtg aggtggggat gggggaggac tggctttccg ccaaggggtca ccaccaccac	2520

caccac

2526

<210> 374

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 374

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190

Ser Asp Asn Leu Ala Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile

675	680	685
Pro Tyr Glu Glu Ala Val	Ala Phe Ile Glu Arg	Tyr Phe Gln Ser Phe
690	695	700
Pro Lys Val Arg Ala Trp	Ile Glu Lys Thr Leu	Glu Glu Gly Arg Lys
705	710	715
Arg Gly Tyr Val	Glu Thr Leu Phe Gly	Arg Arg Arg Tyr Val
725	730	735
Leu Asn Ala Arg	Val Lys Ser Val	Arg Glu Ala Ala Glu
740	745	750
Phe Asn Met Pro	Val Gln Gly Thr Ala	Ala Asp Leu Met
755	760	765
Met Val Lys Leu Phe	Pro Arg Leu Arg	Glu Met Gly Ala
770	775	780
Leu Gln Val Ala	Asn Glu Leu Leu Leu	Glu Ala Pro Gln
785	790	795
Glu Glu Val Ala	Ala Leu Ala Lys Glu	Ala Met Glu Lys
805	810	815
Leu Ala Val Pro	Leu Glu Val Glu	Val Gly Met Gly
820	825	830
Ser Ala Lys Gly	His His His His	His His His
835	840	

<210> 375

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 375

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gaaccggtgc	aggcgggtcta	cggcttcgcc	aagagcctcc	tcaaggccct	gaaggaggac	180
gggtacaagg	ccgtcttcgt	ggtctttgac	gccaaaggccc	cctccttcctg	ccacgaggcc	240
tacgaggcct	acaaggcggg	gagggccccc	acccccgagg	acttcccccg	gcagctcgcc	300
ctcatcaagg	agctggtgga	cctcctgggg	tttaccgcc	tcgaggcccc	cggctacgag	360
gcggacgacg	ttctcgccac	cctggccaag	aaggcggaaa	aggaggggta	cgagggtgcgc	420
atcctcaccg	ccgaccgcga	cctctaccaa	ctcgtctccg	accgcgtcgc	cgctcctccac	480
cccgagggcc	acctcatcac	cccggagtgg	ctttgggaga	agtacggcct	caggccggag	540
cagtgggtgg	acttccgcgc	cctcgtgggg	gacccctccg	acaacctcaa	gggggtcaag	600
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gaagacctca	ggctctcctt	ggagctctcc	cgggtgcgca	ccgacctccc	cctggagggtg	780
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 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340  
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 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460  
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<210> 376

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 376

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
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Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
 50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
 65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
 85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr



100	105	110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu		
115	120	125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala		
130	135	140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His		
145	150	155
		160
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly		
	165	170
		175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro		
	180	185
		190
Ser Asp Asn Leu Lys Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu		
195	200	205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu		
210	215	220
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu		
225	230	235
		240
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu		
	245	250
		255
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly		
	260	265
		270
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu		
275	280	285
Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro		
290	295	300
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro		
305	310	315
		320
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val		
	325	330
		335
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val		
340	345	350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830  
 Ser Ala Lys Gly His His His His His His  
 835 840

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 <223> Synthetic  
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 <400> 378  
 ccgatggagc ctctccga 18  
  
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gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggaggtg	780
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gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc	960
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ttccaaagct tcccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag	2160
cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccacact caacgcccgg	2220
gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccgt ccagggcacc	2280

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gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
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caccac 2526

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<210> 380

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 380

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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
          20           25           30

```

```

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly
35           40           45

```

```

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala
50           55           60

```

```

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala
65           70           75           80

```

```

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro
          85           90           95

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```

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr
          100          105          110

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```

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu
115           120           125

```

```

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala
130           135           140

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Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
 165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Lys Lys Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu



	645		650		655
Ala Val Asp	Pro Leu Met Arg Arg	Ala Ala Lys Thr Val	Asn Phe Gly		
	660	665	670		
Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile					
	675	680	685		
Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe					
	690	695	700		
Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys					
	705	710	715		720
Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp					
	725	730		735	
Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala					
	740	745		750	
Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala					
	755	760		765	
Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu					
	770	775		780	
Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala					
	785	790	795		800
Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro					
	805		810		815
Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu					
	820	825		830	
Ser Ala Lys Gly His His His His His His					
	835	840			

<210> 381

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 381

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33

<210> 382

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 382

gaggtccacc tccaggagga ggtcgggtgcg cac

33

<210> 383

<211> 2526

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

<400> 383

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gaaccgggtgc aggcgggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180

gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc 240

tacgaggcct acaaggcggg gagggccccg acccccaggg acttccccg gcagctcgcc 300

ctcatcaagg agctgggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag 360

gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420

atcctcaccg ccgaccgga cctctaccaa ctcgctctcg accgcgtcgc cgtcctccac 480

cccaggggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540

cagtgggtgg acttcgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag 600

ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660

ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720

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gagttcggca	gcctcctcca	cgagttcggc	ctcctggagg	ccccgcccc	cctggaggag	900
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caccac						2526

<210> 384

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 384

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255

Leu Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met



Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
820 825 830

Ser Ala Lys Gly His His His His His His  
835 840

<210> 385

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 385

ggggccttcg tgggctacgt cctctcccgc ccc

33

<210> 386

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 386

ggggcgggag aggacgtagc ccacgaaggc ccc

33

<210> 387

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 387

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcct ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccaggg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg ttaccgcgc tcgaggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgga cctctaccaa ctcgctctcc accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttcgcgc cctcgtgggg gaccctcctg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggctacg tcctctcccg ccccgagccc	960
atgtggggcg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca	1020



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ctggaggtgg	aggtggggat	gggggaggac	tggctttccg	ccaagggtca	ccaccaccac	2520
caccac						2526

<210> 388

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 388

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240  
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255  
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp



<400> 390  
gttttctggc tttacctggg ccaggtgctt gaggaggttt tc 42

<210> 391

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 391  
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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180  
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgg ccacgaggcc 240  
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300  
ctcatcaagg agctggtgga cctcctgggg tttaccgcc tcgagggtccc cggctacgag 360  
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cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540  
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cgggggtcaag 600  
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ctcaagcacc tggaccaggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720  
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780  
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gaggagggtg	cggctttggc	caaggaggcc	atggagaagg	cctatcccct	cgcctgccc	2460
ctggagggtg	aggtggggat	gggggaggac	tggctttccg	ccaagggtca	ccaccaccac	2520
caccac						2526

<210> 392

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 392

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
 50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
 65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
 85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
 100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
 115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
 130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
 165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu  
 210 215 220

Asp Gln Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270



Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu

515		520		525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys	530	535	540	
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg	545	550	555	560
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly	565	570		575
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr	580	585	590	
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp	595	600	605	
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala	610	615	620	
His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys	625	630	635	640
Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu	645	650	655	
Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly	660	665	670	
Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile	675	680	685	
Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe	690	695	700	
Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys	705	710	715	720
Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp	725	730	735	
Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala	740	745	750	
Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala	755	760	765	

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
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Ser Ala Lys Gly His His His His His His  
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<210> 393

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 393

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33

<210> 394

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 394

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33

<210> 395

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 395

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caccac 2526

<210> 396

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 396

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala

50	55	60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala 65 70 75 80		
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro 85 90 95		
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr 100 105 110		
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu 115 120 125		
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala 130 135 140		
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His 145 150 155 160		
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly 165 170 175		
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro 180 185 190		
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu 195 200 205		
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu 210 215 220		
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu 225 230 235 240		
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu 245 250 255		
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly 260 265 270		
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu 275 280 285		
Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro 290 295 300		

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
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 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
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 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
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 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
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 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
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 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
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Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro



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Ser	Ala	Lys	Gly	His	His	His	His	His	His
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<210> 397

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 397

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33

<210> 398

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 398

caggaggagg tcggtgtgca cccgggagag ctc

33

<210> 399

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 399

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 caccac 2526

<210> 400

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 400

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
 50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
 65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro



His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
820 825 830

Ser Ala Lys Gly His His His His His His

835

840

&lt;210&gt; 401

&lt;211&gt; 2508

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic

&lt;400&gt; 401

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<210> 402

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 402

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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu



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Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly		
35	40	45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala		
50	55	60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala		
65	70	75
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro		
85	90	95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr		
100	105	110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu		
115	120	125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala		
130	135	140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His		
145	150	155
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly		
165	170	175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro		
180	185	190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu		
195	200	205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu		
210	215	220
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu		
225	230	235
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu		
245	250	255
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly		
260	265	270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Val Trp  
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu

770		775		780
Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala				
785		790		795 800
Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro				
	805		810	815
Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu				
	820		825	830
Ser Ala Lys Gly				
	835			

<210> 403

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified\_base

<222> (19)..(51)

<223> The bases in these positions are a synthesis of 91% base shown and 3% all other bases.

<400> 403	
ctccatcgga acctccttaa ggcctcgag ggggaggaga agctcctttg gctctaccac	60
gaggtg	66

<210> 404

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 404

aaggaggttc cgatggag

18

<210> 405

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 405

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgc ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccagag acttccccgc gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaaccgcc tcgagggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgcga cctctaccaa ctcgtctccg accgcgtcgc cgtcctccac	480
cccaggggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcggcc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcggca gcctcctcca cgagttcggc ctcttgaggg ccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc	960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca	1020
gacccttggt cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttggt cctcgaggga ggggctagac ctcgtgcccc gggacgaccc catgctcctc	1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcgggc ctacgggggg	1200
gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc	1260

cttaagcgcc	tcgagggggt	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctcccggg	tcctggccca	tatggaggcc	accggggtac	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
ttggcggggc	accccttcaa	cctcaactcc	cgggaccagc	tggaaagggt	gctctttgac	1500
gagcttaggc	ttcccgctt	gaagaagacg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggcccac	cccatcgtgg	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccccctc	caagcctcgt	ccacccgagg	1680
acgggcccgc	tccacaccog	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
tccgacccca	acctgcagaa	catccccgtc	cgcacccccct	tgggccagag	gatccgccgg	1800
gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgccccat	2040
aggctctccc	aggagcttgc	catcccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	ttcccaaggt	gcgggcctgg	atagaaaaga	ccctggagga	ggggaggaag	2160
cggggctacg	tggaaaccct	cttcggaaga	aggcgctacg	tgcccacact	caacgcccgg	2220
gtgaagagcg	tcagggaggc	cgcggagcgc	atggccttca	acatgcccgt	ccagggcacc	2280
gccgccgacc	tcataagct	cgccatggtg	aagctcttcc	ccgcctccg	ggagatgggg	2340
gcccgcacgc	tcctccaggt	cgccaacgag	ctcctcctgg	aggcccccca	agcgcggggc	2400
gaggaggtgg	cggctttggc	caaggaggcc	atggagaagg	cctatcccct	cgccgtgccc	2460
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<210> 406

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 406

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
 20 25 30  
 Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
 35 40 45  
 Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
 50 55 60  
 Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
 65 70 75 80  
 Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
 85 90 95  
 Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
 100 105 110  
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
 115 120 125  
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
 130 135 140  
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160  
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
 165 170 175  
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190  
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205  
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220  
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240  
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255  
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Val Glu Lys Leu Leu Trp  
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu



515		520		525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys	530	535	540	
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg	545	550	555	560
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly	565	570		575
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr	580	585		590
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp	595	600		605
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala	610	615		620
His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys	625	630	635	640
Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu	645	650		655
Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly	660	665		670
Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile	675	680		685
Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe	690	695	700	
Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys	705	710	715	720
Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp	725	730		735
Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala	740	745		750
Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala	755	760	765	

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830

Ser Ala Lys Gly  
 835

<210> 407

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 407

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcctg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgccg tcgaggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgga cctctaccaa ctcgctctcg accgcgtcgc cgtcctccac	480
cccagaggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gaccctcctg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggaggctg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840

gagttcggca	gcctcctcca	cgagttcggc	ctcctggagg	cccccgcccc	cctggaggag	900
gccccctggc	ccccgccgga	aggggccttc	gtgggcttcg	tcctctcccg	ccccgagccc	960
atgtgggcgg	agcttaaagc	cctggccgcc	tgcaggggcg	gccgcgtgca	ccgggcagca	1020
gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccc	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccgaggggg	tggcgcgggc	ctacgggggg	1200
gagtggacgg	aggacgccgc	ccaccggggc	ctcctctcgg	agaggctcca	tcggaacctc	1260
cttaagcgaa	acgaggggaa	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctcccggg	tcctggccca	tatggaggcc	accggggtag	ggcgggacgt	ggcctacctt	1380
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gagcttaggc	ttcccgcttc	gaagaagacg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggcccac	cccatcgtgg	agaagatcct	ccagcaccgg	1620
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cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacgggtgaac	ttcggcgctc	tctacggcat	gtccgcccac	2040
aggctctccc	aggagcttgc	catcccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	tccccaaagg	gcgggcctgg	atagaaaaga	ccctggagga	ggggaggaag	2160
cggggctacg	tggaaacctc	cttcggaaga	aggcgctacg	tgcccgacct	caacgcccgg	2220
gtgaagagcg	tcagggaggc	cgcggagcgc	atggccttca	acatgcccgt	ccagggcacc	2280
gccgccgacc	tcatagaagc	cgccatggtg	aagctcttcc	cccgcctccg	ggagatgggg	2340
gcccgcacgc	tcctccaggt	cgccaacgag	ctcctcctgg	aggcccccca	agcgcgggcc	2400
gaggaggtgg	cggttttggc	caaggaggcc	atggagaagg	cctatcccct	cgccgtgccc	2460
ctggaggtgg	aggtggggat	gggggaggac	tggctttccg	ccaagggt		2508

<210> 408

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 408

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

His Arg Asn Leu Leu Lys Arg Asn Glu Gly Lys Glu Lys Leu Leu Trp  
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys

705		710		715		720
Arg Gly Tyr Val	Glu Thr Leu Phe Gly	Arg Arg Arg Tyr Val	Pro Asp			
	725	730	735			
Leu Asn Ala Arg Val	Lys Ser Val Arg Glu Ala Ala Glu	Arg Met Ala				
	740	745	750			
Phe Asn Met Pro Val	Gln Gly Thr Ala Ala Asp	Leu Met Lys Leu Ala				
	755	760	765			
Met Val Lys Leu Phe Pro	Arg Leu Arg Glu Met Gly Ala Arg Met Leu					
	770	775	780			
Leu Gln Val Ala Asn Glu Leu Leu Leu Glu	Ala Pro Gln Ala Arg Ala					
	785	790	795	800		
Glu Glu Val Ala Ala Leu Ala Lys Glu	Ala Met Glu Lys Ala Tyr Pro					
	805	810	815			
Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu						
	820	825	830			
Ser Ala Lys Gly						
	835					

<210> 409

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 409

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
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<210> 410

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 410

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
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Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
 165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
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Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Phe Glu Gly Glu Glu Lys Leu Leu Cys  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
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 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
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 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
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 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu



<223> Synthetic

<400> 411

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<210> 412

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 412

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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro

				85					90					95	
Arg	Gln	Leu	Ala 100	Leu	Ile	Lys	Glu	Leu 105	Val	Asp	Leu	Leu	Gly 110	Phe	Thr
Arg	Leu	Glu 115	Val	Pro	Gly	Tyr	Glu 120	Ala	Asp	Asp	Val	Leu 125	Ala	Thr	Leu
Ala	Lys 130	Lys	Ala	Glu	Lys	Glu 135	Gly	Tyr	Glu	Val	Arg 140	Ile	Leu	Thr	Ala
Asp 145	Arg	Asp	Leu	Tyr	Gln 150	Leu	Val	Ser	Asp	Arg 155	Val	Ala	Val	Leu	His 160
Pro	Glu	Gly	His	Leu 165	Ile	Thr	Pro	Glu	Trp 170	Leu	Trp	Glu	Lys	Tyr 175	Gly
Leu	Arg	Pro	Glu 180	Gln	Trp	Val	Asp	Phe 185	Arg	Ala	Leu	Val	Gly 190	Asp	Pro
Ser	Asp	Asn 195	Leu	Pro	Gly	Val	Lys 200	Gly	Ile	Gly	Glu	Lys 205	Thr	Ala	Leu
Lys	Leu 210	Leu	Lys	Glu	Trp	Gly 215	Ser	Leu	Glu	Asn	Leu 220	Leu	Lys	Asn	Leu
Asp 225	Arg	Val	Lys	Pro	Glu 230	Asn	Val	Arg	Glu	Lys 235	Ile	Lys	Ala	His	Leu 240
Glu	Asp	Leu	Arg	Leu 245	Ser	Leu	Glu	Leu	Ser 250	Arg	Val	Arg	Thr	Asp 255	Leu
Pro	Leu	Glu	Val 260	Asp	Leu	Ala	Gln	Gly 265	Arg	Glu	Pro	Asp	Arg 270	Glu	Gly
Leu	Arg	Ala 275	Phe	Leu	Glu	Arg	Leu 280	Glu	Phe	Gly	Ser	Leu 285	Leu	His	Glu
Phe	Gly 290	Leu	Leu	Glu	Ala	Pro 295	Ala	Pro	Leu	Glu	Glu 300	Ala	Pro	Trp	Pro
Pro 305	Pro	Glu	Gly	Ala	Phe 310	Val	Gly	Phe	Val	Leu 315	Ser	Arg	Pro	Glu	Pro 320
Met	Trp	Ala	Glu	Leu 325	Lys	Ala	Leu	Ala	Ala 330	Cys	Arg	Gly	Gly	Arg 335	Val

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Phe Leu Lys Lys Thr Lys Lys  
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Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590



Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
           595                                600                                605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
           610                                615                                620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
   625                                630                                635                                640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
                                 645                                650                                655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
                                 660                                665                                670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
           675                                680                                685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
           690                                695                                700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
   705                                710                                715                                720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
                                 725                                730                                735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
                                 740                                745                                750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
           755                                760                                765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
   770                                775                                780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
   785                                790                                795                                800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
                                 805                                810                                815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
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Ser Ala Lys Gly

835

<210> 413

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc\_feature

<222> (19)..(21)

<223> n is any base a,t,c, or g.

<400> 413

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42

<210> 414

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

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<400> 414

cctaagctcg tcaaagag

18

<210> 415

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<212> DNA

<213> Artificial Sequence

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<210> 416

<211> 836

<212> PRT

<213> Artificial Sequence .

<220>

<223> Synthetic

<400> 416

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
 50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
 65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
 85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
 100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
 115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
 130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
 165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Val Leu Lys Lys Thr Lys Lys  
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp

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Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala
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His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys
625					630					635					640
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu
				645					650					655	
Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly
			660					665					670		
Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile
		675					680					685			
Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe
	690					695					700				
Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys
705					710					715					720
Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp
				725					730					735	
Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala
			740					745					750		
Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala
		755					760					765			
Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu
	770					775					780				
Leu	Gln	Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala
785					790					795					800
Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro
			805						810					815	
Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu
			820					825					830		
Ser	Ala	Lys	Gly												
		835													

<210> 417

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 417

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gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgg ccacgaggcc      240
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gcggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgagggtgcg      420
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 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460  
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<210> 418

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 418

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly

35					40					45					
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
50						55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75					80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
			100					105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
145					150					155					160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu
	210					215					220				
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu
225					230					235					240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu
				245					250					255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly
			260					265					270		
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu
		275					280					285			

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
290 295 300  
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
305 310 315 320  
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
325 330 335  
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
340 345 350  
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
355 360 365  
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
370 375 380  
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
385 390 395 400  
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
405 410 415  
His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
420 425 430  
Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
435 440 445  
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
450 455 460  
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
465 470 475 480  
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
485 490 495  
Val Leu Phe Asp Glu Leu Arg Leu Pro Ser Leu Lys Lys Thr Lys Lys  
500 505 510  
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
515 520 525  
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala

785		790		795		800									
Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro
			805					810						815	
Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu
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Ser	Ala	Lys	Gly												
		835													

<210> 419  
 <211> 2508  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 419  
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<210> 420

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 420

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480



Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
500 505 510

Thr Gly Lys Arg Ser Thr Gly Ala Ala Val Leu Glu Ala Leu Arg Glu  
515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp

725					730					735					
Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala
			740					745					750		
Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala
		755					760					765			
Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu
	770					775					780				
Leu	Gln	Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala
	785					790					795				800
Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro
			805					810						815	
Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu
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Ser	Ala	Lys	Gly												
		835													

<210> 421

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc\_feature

<222> (16)..(18)

<223> n is any base a,t,c, or g.

<400> 421

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42

<210> 422

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 422

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15

<210> 423

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 423

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcctg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccc acccccgagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag	360
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cagtgggtgg acttccgcgc cctcgtgggg gaccctcccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
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gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggaggctg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
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<210> 424

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 424

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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
225 230 235 240



485										490					495				
Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys				
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Thr	Gly	Lys	Arg	Ser	Thr	Ser	Leu	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu				
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Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys				
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Leu	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg				
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Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr				
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Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp				
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625					630					635					640				
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu				
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Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly				
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Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile				
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Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe				
	690					695					700								
Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys				
705					710					715					720				
Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp				
				725					730					735					

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
820 825 830

Ser Ala Lys Gly  
835

<210> 425

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> n

<222> (19) .. (21)

<223> n is any base a,t,c, or g.

<220>

<221> misc\_feature

<222> (19) .. (21)

<223> n is any base a,t,c, or g.



<400> 425  
ggcaagcgct ccaccagcnn ngcgggtgctg gaggccctac gg 42

<210> 426

<211> 2508

<212> DNA

<213> Artificial Sequence

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<210> 427

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 427

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20	25	30
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly		
35	40	45
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala		
50	55	60
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala		
65	70	75
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro		
85	90	95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr		
100	105	110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu		
115	120	125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala		
130	135	140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His		
145	150	155
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly		
165	170	175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro		
180	185	190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu		
195	200	205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu		
210	215	220
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu		
225	230	235
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu		
245	250	255
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly		
260	265	270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Arg Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu

770

775

780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830

Ser Ala Lys Gly  
 835

<210> 428

<211> 2499

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 428

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gaggagggcg	gggagcgggc	cgccttttcc	gagaggctct	tcgccaacct	gcttaagagg	1260
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gcccggctgg	ccaaggaggt	catggagggg	gtgtatcccc	tggccgtgcc	cctggaggtg	2460
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<210> 429

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 429

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	
			20					25					30			
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	
		35					40					45				
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	
	50					55					60					
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	
65					70					75					80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	
				85					90					95		
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	
			100					105					110			
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	
		115					120					125				
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	
	130					135					140					
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	
145					150					155					160	
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	
				165					170					175		
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	
		180						185					190			
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	
		195					200					205				



Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460

Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Gln Lys Thr Gly Lys  
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr

705		710		715		720									
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala
				725					730					735	
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met
			740					745					750		
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys
		755					760					765			
Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val
	770					775					780				
Ala	Asn	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val
785					790					795					800
Ala	Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val
			805						810					815	
Pro	Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys
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Glu

<210> 430

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 430

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27

<210> 431

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 431

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gaaccggtgc	aggcgtcta	cggcttcgcc	aagagcctcc	tcaaggccct	gaaggaggac	180
gggtacaagg	ccgtcttcgt	ggtctttgac	gccaaaggccc	cctccttcct	ccacgaggcc	240
tacgaggcct	acaaggcggg	gaggggccccg	acccccgagg	acttcccccg	gcagctcgcc	300
ctcatcaagg	agctggtgga	cctcctgggg	tttaccgcgc	tcgagggtccc	cggctacgag	360
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atcctcaccg	ccgaccgcca	cctctaccaa	ctcgtctccg	accgcgtcgc	cgctctccac	480
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ggcatcgggg	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaagcct	ggaaaacctc	660
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acgggcccgc	tccacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740

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 ctgatgcgcc gggcggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac 2040  
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 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt 2508

<210> 432

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 432

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
 50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
 65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
 85 90 95  
 Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
 100 105 110  
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
 115 120 125  
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
 130 135 140  
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160  
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
 165 170 175  
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190  
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205  
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220  
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240  
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255  
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Lys Leu Lys Lys Thr Lys Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr

580					585					590					
Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp
		595					600					605			
Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala
		610				615					620				
His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys
		625				630					635				640
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu
				645					650					655	
Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly
			660					665					670		
Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile
		675					680					685			
Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe
	690					695					700				
Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys
	705					710					715				720
Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp
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Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala
			740					745					750		
Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala
		755					760					765			
Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu
	770					775					780				
Leu	Gln	Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala
	785					790					795				800
Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro
				805					810					815	
Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu
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Ser Ala Lys Gly  
835

<210> 433

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 433

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36

<210> 434

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 434

tgtcttcttc gtcttcttca acttggaag cctaag

36

<210> 435

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 435

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ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc

120

gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggcct gaaggaggac

180

gggtacaagg ccgtcttcgt ggtctttgac gccaaagccc cctccttcg ccacgaggcc

240

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gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatcgcca	cccagaccgc	aagctggatg	ttcggcgctc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgctc	tctacggcat	gtccgcccac	2040
aggctctccc	aggagcttgc	catccccctac	gaggaggcgg	tggcctttat	agagcgctac	2100

ttccaaagct tccccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160  
 cggggctacg tggaaccct cttcggaaga aggcgctacg tgcccgcacct caacgcccgg 2220  
 gtgaagagcg tcaggaggc cgcgagcgc atggccttca acatgcccgt ccagggcacc 2280  
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340  
 gcccgcatgc tctccaggt cgccaacgag ctctctctgg agggccccca agcgcgggcc 2400  
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460  
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt 2508

<210> 436

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 436

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
 1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
 50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
 65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
 85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
 100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
 115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
 130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
 165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys

625		630		635		640									
Asp	Ile	Ala	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu
				645					650					655	
Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly
			660					665					670		
Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile
		675					680					685			
Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe
	690					695					700				
Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys
	705				710					715					720
Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp
				725					730					735	
Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala
			740					745					750		
Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala
		755					760					765			
Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu
	770					775					780				
Leu	Gln	Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala
	785				790					795					800
Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro
			805						810					815	
Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu
			820					825					830		
Ser	Ala	Lys	Gly												
		835													

<210> 437

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 437  
gaggggaagg acatcgccac ccagaccgca agc 33

<210> 438

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 438  
gcttgcggtc tgggtggcga tgtccttccc ctc 33

<210> 439

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 439  
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60  
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120  
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180  
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgg ccacgaggcc 240  
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300  
ctcatcaagg agctggtgga cctcctgggg ttaccgcgc tcgagggtccc cggctacgag 360  
gcggaacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgagggtgcgc 420  
atcctcaccg ccgaccgcga cctctaccaa ctcgtctccg accgcgtcgc cgtcctccac 480  
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540  
cagtgggtgg acttcgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag 600

ggcatcgggg	agaagaccgc	cctcaagctc	ctcaaggagt	ggggaagcct	ggaaaacctc	, 660
ctcaagaacc	tggaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggcccacctg	720
gaagacctca	ggctctcctt	ggagctctcc	cgggtgcgca	ccgacctccc	cctggagggtg	780
gacctcgccc	aggggcggga	gcccgaccgg	gaggggctta	gggccttcct	ggagaggctg	840
gagttcggca	gcctcctcca	cgagttcggc	ctcctggagg	ccccgcgcc	cctggaggag	900
gccccctggc	ccccgcggga	aggggccttc	gtgggcttcg	tcctctcccg	ccccgagccc	960
atgtggggcg	agcttaaagc	cctggccgcc	tgcaggggcg	gccgcgtgca	ccgggcagca	1020
gaccccttgg	cggggctaaa	ggacctcaag	gaggtccggg	gcctcctcgc	caaggacctc	1080
gccgtcttgg	cctcgaggga	ggggctagac	ctcgtgcccg	gggacgaccc	catgctcctc	1140
gcctacctcc	tggacccttc	gaacaccacc	cccgaggggg	tggcgcggcg	ctacgggggg	1200
gagtggaagg	aggacgccgc	ccaccgggcc	ctcctctcgg	agaggctcca	tcggaacctc	1260
cttaagcgcc	tcgaggggga	ggagaagctc	ctttggctct	accacgaggt	ggaaaagccc	1320
ctctcccggg	tcctggccca	tatggaggcc	accggggtac	ggcgggacgt	ggcctacctt	1380
caggcccttt	ccctggagct	tgcggaggag	atccgccgcc	tcgaggagga	ggtcttccgc	1440
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gagcttaggc	ttcccgctt	gaagaagccg	aagaagacag	gcaagcgctc	caccagcgcc	1560
gcggtgctgg	aggccctacg	ggaggcccac	cccatcgtag	agaagatcct	ccagcaccgg	1620
gagctcacca	agctcaagaa	cacctacgtg	gacccctccc	caagcctcgt	ccacccgagg	1680
acgggcccgc	tccacacccg	cttcaaccag	acggccacgg	ccacggggag	gcttagtagc	1740
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gccttcgtgg	ccgaggcggg	ttgggcgttg	gtggccctgg	actatagcca	gatagagctc	1860
cgcgtcctcg	cccacctctc	cggggacgaa	aacctgatca	gggtcttcca	ggaggggaag	1920
gacatccaca	cccagaccgc	aagctggatg	ttcggcgtcc	ccccggaggc	cgtggacccc	1980
ctgatgcgcc	gggcggccaa	gacggtgaac	ttcggcgtcc	tctacggcat	gtccgcccat	2040
aggctctccc	aggagcttgc	catcccctac	gaggaggcgg	tggcctttat	agagcgctac	2100
ttccaaagct	ttcccaaggt	gcgggcctgg	atagaaaaga	ccctggagga	ggggaggaag	2160
cggggctacg	tggaaaccct	cttcggaaga	aggcgctacg	tgcccgaacct	caacgcccgg	2220
gtgaagagcg	tcagggaggc	cgcggagcgc	atggccttca	acatgcccgt	ccagggcacc	2280
gccgccgacc	tcatgaagct	cgccatggtg	aagctcttcc	ccgcctccg	ggagatgggg	2340
gcccgcacgc	tcctccaggt	cgccaacgag	ctcctcctgg	agggccccca	agcgcggggc	2400
gaggagggtg	cggctttggc	caaggaggcc	atggagaagg	cctatcccct	cgcctgcccc	2460



ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggg

2508

<210> 440

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 440

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Pro Lys Lys  
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile

675	680	685
Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe		
690	695	700
Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys		
705	710	715
Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp		
	725	730
		735
Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala		
	740	745
		750
Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala		
	755	760
		765
Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu		
	770	775
		780
Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala		
785	790	795
		800
Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro		
	805	810
		815
Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu		
	820	825
		830
Ser Ala Lys Gly		
	835	

<210> 441

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 441

cccgccttga agaagccgaa gaagacaggc aag

33

<210> 442

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 442

cttgccctgtc ttcttcggct tcttcaaggc ggg

33

<210> 443

<211> 2499

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 443

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caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag	120
ccggtgcagg cgggtctacgg cttegccaag agcctcctca aggcctcaa ggaggacggg	180
gacgcggtga tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggcctacggg	240
gggtacaagg cgggcccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc	300
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccag	480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg	540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc	600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag	660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg	720
aagctctcct gggacctggc caagggtgcg accgacctgc ccctggagggt ggacttcgcc	780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttgcc	840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg	900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc	960

gatcttcttg	ccctggccgc	cgccaggggc	ggccgcgttt	accgggcgga	ggatcccttg	1020
gaggccttgc	gggggcttgg	ggaggtgagg	gggcttttgg	ccaaggacct	ggcggtgctg	1080
gccctgaggg	aagggattgc	cctggcaccg	ggcgacgacc	ccatgctcct	cgcttacctc	1140
ctggatcctt	ccaacaccgc	ccccgaagg	gtagcccggc	gctacggggg	ggagtggacc	1200
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catcctttca	acctgaactc	ccgggaccag	ctggaaagg	tcatctttga	cgagcttggg	1500
cttcccgcga	tcaagaagac	gaggaagacg	ggcaagcgct	ccaccagcgc	cgccgttttg	1560
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aagctcaagg	gaacctacat	cgatcccttg	cctgccctgg	tccaccccaa	gacgaaccgc	1680
ctccacaccc	gtttcaacca	gacggccacc	gccacgggga	ggcttagcag	ctcggatcct	1740
aatctgcaaa	atatccccgt	gcgacccct	ttggggccagc	ggatccgccc	ggccttcgtg	1800
gccgaggagg	ggtggaggct	ggtggttttg	gactacagcc	agattgagct	cagggtcctg	1860
gcgcaccttt	ccggggacga	gaacctaatc	cggtcttcc	aggagggcca	ggacatccac	1920
accagacgg	ccagctggat	gttcggcggtg	ccccagagg	ccgtggattc	cctgatgcgc	1980
cgggcggcca	agaccatcaa	cttcggcgtc	ctctacggca	tgtccgcca	ccggctttcg	2040
ggagagctgg	ccatcccccta	cgaggaggcg	gtggccttca	tcgagcggtg	tttcagagc	2100
tacccaagg	tgcgggcctg	gattgagaaa	accctggcgg	aaggacggga	acggggctat	2160
gtggaaaccc	tctttggccg	ccggcgctac	gtgcccgaact	tggcttccc	ggtgaagagc	2220
atccgggagg	cagcggagcg	catggccttc	aacatgcgg	tccaggggac	cgccgcggat	2280
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cttttgagg	tgcacaacga	actggctctc	gaggctccca	aggagcaagc	ggaggaagtc	2400
gcccaggagg	ccaagcggac	catggaggag	gtgtggcccc	tgaagggtgc	cttggagggtg	2460
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<210> 444

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 444

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val Tyr Arg Ala  
 325 330 335  
 Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu  
 355 360 365  
 Ala Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala  
 405 410 415  
 Leu Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val  
 450 455 460  
 Glu Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg Leu Ala Gly  
 465 470 475 480



His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Ile Phe  
485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Arg Lys Thr Gly Lys  
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
515 520 525

Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly  
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg  
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val  
595 600 605

Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His  
625 630 635 640

Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
645 650 655

Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu  
675 680 685

Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val  
690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr  
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser

	725		730		735
Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met	740		745		750
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys	755		760		765
Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val	770		775		780
His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val	785		790		795
					800
Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val		805		810	815
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys		820		825	830
Ala					

<210> 445

<211> 2496

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 445

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ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg	180
gacgcggtga tcgtggtcct tgacgccaag gccccctcct tccgccacga ggcctacggg	240
gggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc	300
aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc	420
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gggtacctca	tcaccccggc	ctggctttgg	gaaaagtacg	gcctgaggcc	cgaccagtgg	540
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cccccgccgg	aaggggcctt	cgtgggcttt	gtgctttccc	gcaaggagcc	catgtggggc	960
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gaggccctgg	ccgacctcaa	ggaggcccgg	gggttcctgg	ccaaggacct	ggccgttttg	1080
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gccacatgg	aggcccgggg	ggtgaggctg	gacgtccccc	ttctggaggc	cctctccttt	1380
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accgccgcct	ggatgttcgg	cttagacccc	gctctggtgg	atccaaagat	gcgccggggcg	1980
gccaagacgg	tcaacttcgg	cgtcctctac	gggatgtccg	cccacaggct	ctcccaggag	2040
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aaggtgcggg	cctggataga	aaggaccctg	gaggaggggc	ggacgcgggg	ctacgtggag	2160
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gaggcggcgg	agcggatggc	cttcaacatg	cccgtgcagg	gcaccgccgc	cgacctgatg	2280
aagatcgcca	tgggtcaagct	cttccccagg	ctaaagcccc	tgggggcccc	cctcctcctc	2340

caagtggcca acgagctggg cctggagggtg cccgaggacc gggccgagga ggccaaggcc 2400  
 ctgggtcaagg aggtcatgga gaacgcctac cccctggacg tgcccctcga ggtggagggtg 2460  
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<210> 446

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 446

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335

Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala Arg Gly Phe  
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Val Ala Leu  
 355 360 365

Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu Asp Pro Ala  
 370 375 380

Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Phe Thr  
 385 390 395 400

Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Gln Asn  
 405 410 415

Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr Gln Glu Val  
420 425 430

Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Arg Gly Val  
435 440 445

Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu Leu Glu Lys  
450 455 460

Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala Gly His Pro  
465 470 475 480

Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu  
485 490 495

Leu Gly Leu Thr Pro Val Lys Arg Thr Lys Lys Thr Gly Lys Arg Ser  
500 505 510

Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His Pro Ile Val  
515 520 525

Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Ser Thr Tyr  
530 535 540

Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly Arg Leu His  
545 550 555 560

Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser  
565 570 575

Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg  
580 585 590

Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu Leu Ala Ala  
595 600 605

Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp  
610 615 620

Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile His Thr Glu  
625 630 635 640

Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val Asp Pro Lys  
645 650 655

Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met

660	665	670
Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr Lys Glu Ala		
675	680	685
Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala		
690	695	700
Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly Tyr Val Glu		
705	710	715
Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg Val		
725	730	735
Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val		
740	745	750
Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val Lys Leu Phe		
755	760	765
Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln Val Ala Asn		
770	775	780
Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu Ala Lys Ala		
785	790	795
Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp Val Pro Leu		
805	810	815
Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala Lys Gln Asp		
820	825	830

<210> 447

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 447

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gaaccggtgc	aggcgggtcta	cggcttcgcc	aagagcctcc	tcaaggccct	gaaggaggac	180
gggtacaagg	ccgtcttcgt	ggtctttgac	gccaaggccc	cctccttccg	ccacgaggcc	240
tacgaggcct	acaaggcggg	gagggccccg	acccccgagg	acttcccccg	gcagctcgcc	300
ctcatcaagg	agctggtgga	cctcctgggg	tttaccgcc	tcgaggcccc	cggctacgag	360
gcggacgacg	ttctcgccac	cctggccaag	aaggcggaaa	aggaggggta	cgagggtgcgc	420
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cccgagggcc	acctcatcac	cccggagtgg	ctttgggaga	agtacggcct	caggccggag	540
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ctcaagaacc	tggaccgggt	aaagccagaa	aacgtccggg	agaagatcaa	ggccccacctg	720
gaagacctca	ggctctcctt	ggagctctcc	cgggtgcgca	ccgacctccc	cctggagggtg	780
gacctcgccc	aggggcggga	gcccgaccgg	gaggggctta	gggccttcct	ggagaggctg	840
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gatcccttgg	aggccttgcg	ggggcttggg	gaggtgaggg	ggcttttggc	caaggacctg	1080
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gccttcgtgg	ccgaggaggg	gtggaggctg	gtggttttgg	actacagcca	gattgagctc	1860
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gacatccaca	cccagacggc	cagctggatg	ttcggcgctg	ccccagaggc	cgtggattcc	1980



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 ttccagagct accccaaggt gcgggccttg attgagaaaa ccctggcgga aggacgggaa 2160  
 cggggctatg tggaaaccct ctttggccgc cggcgctacg tgcccgaactt ggcttcccgg 2220  
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 gccgcggatt tgatgaaact ggccatggtg aagctctttc ccaggcttca ggagctgggg 2340  
 gccaggatgc ttttgcaggt gcacaacgaa ctggctctcg aggctcccaa ggagcaagcg 2400  
 gaggaagtgc cccaggaggc caagcggacc atggaggagg tgtggcccct gaaggtgccc 2460  
 ttggagggtg aagtgggcat cggggaggac tggctttccg ccaaggcc 2508

<210> 448

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 448

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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
 50 55 60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
 65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
 85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
 100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
 115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
 130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
 165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335

Tyr Arg Ala Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly  
 355 360 365

Ile Ala Leu Ala Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

Tyr Ala Ala Leu Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp  
 420 425 430

Leu Tyr Glu Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445

Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser  
 450 455 460

Leu Glu Val Glu Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg  
 465 470 475 480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495

Val Ile Phe Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Arg Lys  
 500 505 510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525

Ala His Pro Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys  
 530 535 540

Leu Lys Gly Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys  
 545 550 555 560

Thr Asn Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp  
 595 600 605

Arg Leu Val Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala

610	615	620
His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln 625                      630                      635                      640		
Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu 645                      650                      655		
Ala Val Asp Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly 660                      665                      670		
Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile 675                      680                      685		
Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr 690                      695                      700		
Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu 705                      710                      715                      720		
Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp 725                      730                      735		
Leu Ala Ser Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala 740                      745                      750		
Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala 755                      760                      765		
Met Val Lys Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu 770                      775                      780		
Leu Gln Val His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala 785                      790                      795                      800		
Glu Glu Val Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro 805                      810                      815		
Leu Lys Val Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu 820                      825                      830		
Ser Ala Lys Ala 835		
<210> 449		
<211> 2505		

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 449

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac      180
gggtacaagg ccgtcttcgt ggtctttgac gccaaagccc cctccttcg ccacgaggcc      240
tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc      300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag      360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc      420
atcctcaccg ccgaccgga cctctaccaa ctcgctccg accgcgtcgc cgtcctccac      480
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Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala

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Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro		85	90	95
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr		100	105	110
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu		115	120	125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala		130	135	140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His	145	150	155	160
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly		165	170	175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro		180	185	190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu		195	200	205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu		210	215	220
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu	225	230	235	240
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu		245	250	255
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly		260	265	270
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Leu Glu Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala  
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Phe Asp Glu Leu Gly Leu Thr Pro Val Lys Arg Thr Lys Lys Thr Gly  
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Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly  
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<211> 842

<212> PRT

<213> Artificial Sequence

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<400> 456

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 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
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 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160  
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
 165 170 175  
 Leu Lys Pro Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro  
 180 185 190  
 Ser Asp Asn Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala  
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 Lys Leu Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu  
 210 215 220  
 Glu Gln Val Lys Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met  
 225 230 235 240  
 Glu Asp Leu Lys Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu  
 245 250 255  
 Leu Leu Gln Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Lys Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285



Phe Gly Leu Leu Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro  
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Pro Pro Glu Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro  
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Met Trp Ala Glu Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val  
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
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Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
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Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495

Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
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Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
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Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys

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Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly
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Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr
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Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp
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Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu
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Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile
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Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys
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Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp
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Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala
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Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala
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Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu
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Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
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Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
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Ser Ala Lys Gly His His His His His His  
835 840

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<223> Synthetic

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<212> DNA

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<400> 458

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<210> 459

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<223> Synthetic

<400> 459

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ctcatcaagg agctgggtgga cctcctgggg tttaccgcc tcgagggtccc cggctacgag	360
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<211> 842

<212> PRT

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			20					25					30		

Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			

Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				

Val	Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
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65		70		75		80									
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Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
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Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
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Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
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Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
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Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
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Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
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Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu
	210					215					220				
Glu	Gln	Val	Lys	Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met
225					230					235					240
Glu	Asp	Leu	Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Asp	Leu
				245					250					255	
Leu	Leu	Gln	Val	Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly
			260					265					270		
Leu	Lys	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu
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Phe	Gly	Leu	Leu	Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro
	290					295					300				
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro
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Met Trp Ala Glu Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val  
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 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
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 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
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 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
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 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu



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<211> 844

<212> PRT

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Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60

Val Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr

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Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu		
115	120	125
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala		
130	135	140
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His		
145	150	155
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly		
165	170	175
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro		
180	185	190
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu		
195	200	205
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu		
210	215	220
Asp Arg Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu		
225	230	235
Glu Asp Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu		
245	250	255
Pro Leu Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu		
260	265	270
Glu Gly Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu		
275	280	285
His Glu Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro		
290	295	300
Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys		
305	310	315
Glu Pro Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly		
325	330	335
Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys		
340	345	350

Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg  
 355 360 365

Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr  
 370 375 380

Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr  
 385 390 395 400

Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu  
 405 410 415

Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu  
 420 425 430

Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala  
 435 440 445

His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala  
 450 455 460

Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val  
 465 470 475 480

Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu  
 485 490 495

Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr  
 500 505 510

Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu  
 515 520 525

Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu  
 530 535 540

Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His  
 545 550 555 560

Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala  
 565 570 575

Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val  
 580 585 590

Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala  
 595 600 605

Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val  
610 615 620

Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu  
625 630 635 640

Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro  
645 650 655

Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn  
660 665 670

Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu  
675 680 685

Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln  
690 695 700

Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly  
705 710 715 720

Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val  
725 730 735

Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg  
740 745 750

Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys  
755 760 765

Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg  
770 775 780

Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala  
785 790 795 800

Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala  
805 810 815

Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp  
820 825 830

Trp Leu Ser Ala Lys Gly His His His His His His  
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 tacgaggcct acaaggcggg gagggccccc acccccagagg acttcccccg gcagctcgcc 300  
 ctcatcaagg agctggtgga cctcctgggg tttaccgccg tcgaggtccc cggctacgag 360  
 gcggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgaggtgcgc 420

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gcccataggc	tctcccagga	gcttgccatc	ccctacgagg	aggcgggtggc	ctttatagag	2100
cgctacttcc	aaagcttccc	caaggtgcgg	gcctggatag	aaaagaccct	ggaggagggg	2160
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gcccgggtga	agagcgtcag	ggaggccgcg	gagcgcatgg	ccttcaacat	gcccgtccag	2280



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cgggccgagg aggtggcggc tttggccaag gaggccatgg agaaggccta tcccctcgcc 2460  
gtgcccctgg aggtggaggt ggggatgggg gaggactggc tttccgcaa gggtcaccac 2520  
caccaccacc ac 2532

<210> 468

<211> 844

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 468

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75				80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
			100					105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160  
 Pro Glu Gly His Leu Ile Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly  
 165 170 175  
 Val Pro Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg  
 180 185 190  
 Ser Asp Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205  
 Arg Leu Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu  
 210 215 220  
 Asp Arg Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu  
 225 230 235 240  
 Glu Asp Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu  
 245 250 255  
 Pro Leu Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu  
 260 265 270  
 Glu Gly Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu  
 275 280 285  
 His Glu Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro  
 290 295 300  
 Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys  
 305 310 315 320  
 Glu Pro Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly  
 325 330 335  
 Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys  
 340 345 350  
 Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg  
 355 360 365  
 Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr  
 370 375 380  
 Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr  
 385 390 395 400

Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu  
405 410 415

Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu  
420 425 430

Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala  
435 440 445

His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala  
450 455 460

Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val  
465 470 475 480

Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu  
485 490 495

Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr  
500 505 510

Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu  
515 520 525

Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu  
530 535 540

Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His  
545 550 555 560

Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala  
565 570 575

Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val  
580 585 590

Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala  
595 600 605

Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val  
610 615 620

Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu  
625 630 635 640

Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro



<223> Synthetic

<400> 469

ctcgaggcgg gtaaacccca ggaggtc

27

<210> 470

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 470

gggtttaccc gcctcgaggc gcccggc

27

<210> 471

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 471

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ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120

gaaccgggtgc aggcgggtcta cggtctcgcc aagagcctcc tcaaggccct gaaggaggac 180

gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttcg ccacgaggcc 240

tacgaggcct acaaggcggg gagggccccg acccccgagg acttccccg gcagctcgcc 300

ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtgcc gggctttgaa 360

gcggatgacg tcctggctac cctggccaag aaggcggaaa aggaaggcta cgaagtgcgc 420

atcctcaccg cggaccggga cctttaccag cttctttcgg agcgaatctc catccttcac 480

ccggaggggtt acctgatcac ccgggagtggt ctttgggaga agtatgggct taagccttcc 540

cagtgggttg actaccgggc cttggccggg gacccttcg acaacatccc cggcgtgaag 600

ggcatcgggg agaagacggc ggccaagctg atccgggagt ggggaagcct ggaaaacctt 660

cttaagcacc tggaacaggc gaaacctgcc tccgtgcggg agaagatcct tagccacatg 720

gaggacctca agctatccct ggagctatcc cgggtgcaca cggacttgct ccttcaggtg	780
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caccac	2526

<210> 472

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 472

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60

Val Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110

Arg Leu Glu Val Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His  
145 150 155 160

Pro Glu Gly Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175

Leu Lys Pro Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro  
180 185 190

Ser Asp Asn Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala  
 195 200 205

Lys Leu Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu  
 210 215 220

Glu Gln Val Lys Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met  
 225 230 235 240

Glu Asp Leu Lys Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu  
 245 250 255

Leu Leu Gln Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly  
 260 265 270

Leu Lys Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285

Phe Gly Leu Leu Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro  
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val  
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met



435	440	445
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser		
450	455	460
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg		
465	470	475
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg		
485	490	495
Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys		
500	505	510
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu		
515	520	525
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys		
530	535	540
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg		
545	550	555
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly		
565	570	575
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr		
580	585	590
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp		
595	600	605
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala		
610	615	620
His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys		
625	630	635
Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu		
645	650	655
Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly		
660	665	670
Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile		
675	680	685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
820 825 830

Ser Ala Lys Gly His His His His His His  
835 840

<210> 473

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 473

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27

<210> 474

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 474

atcacccccgg agtggctttg ggagaag

27

<210> 475

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 475

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caggcggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg	180
gtgatcgtgg tctttgacgc cgaggccccc tccttcgcgc accagacctt cgaggcctac	240
aaggcggggc gggtctccac ccccgaggac ttccccggc agcttgccct tatcaaggag	300
atggtggacc ttttgggcct ggagcgcctc gaggtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaaaag gaaggctacg aagtgcgcac cctcaccgcg	420
gaccgggacc tttaccagct tctttcggag cgaatctcca tccttcaccc ggaggggttac	480
ctgatcaccc cggagtggct ttgggagaag tacggcctca ggccggagca gtgggtggac	540
ttccgcgccc tcgtggggga cccctccgac aacctccccg ggggtcaagg catcggggag	600
aagaccgccc tcaagctcct caaggagtgg ggaagcctgg aaaacctcct caagaacctg	660
gaccgggtaa agccagaaaa cgtccgggag aagatcaagg ccacacctga agacctcagg	720
ctctccttgg agctctcccg ggtgcgcacc gacctcccc tggaggtgga cctcgcccag	780
gggcgggagc ccgaccggga ggggcttagg gccttcctgg agaggctgga gttcggcagc	840
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ccgccggaag gggccttcgt gggcttcgtc ctctcccgc cagagcccat gtgggcggag	960
cttaaagccc tggccgcctg caggggcggc cgcgtgcacc gggcagcaga ccccttggcg	1020

gggctaaagg	acctcaagga	gtccggggc	ctcctcgcca	aggacctcgc	cgtcttggcc	1080
tcgagggagg	ggctagacct	cgtgcccggg	gacgaccca	tgctcctcgc	ctacctcctg	1140
gacccttcga	acaccacccc	cgaggggggtg	gcgcggcgct	acggggggga	gtggacggag	1200
gacgccgccc	accggggcct	cctctcggag	aggctccatc	ggaacctcct	taagcgctc	1260
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<210> 476

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 476

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Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys  
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val  
50 55 60

Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr  
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val  
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala  
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu  
130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr  
145 150 155 160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Glu  
165 170 175

Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp Asn Leu  
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu Leu Lys  
195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val Lys  
210 215 220

Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp Leu Arg  
225 230 235 240

Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val  
 245 250 255  
 Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe  
 260 265 270  
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285  
 Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300  
 Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
 305 310 315 320  
 Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg Ala Ala  
 325 330 335  
 Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu  
 340 345 350  
 Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu  
 405 410 415  
 Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu  
 420 425 430  
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala  
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 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His  
 465 470 475 480  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp

485										490					495				
Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys	Arg				
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Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile				
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Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn	Thr				
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Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	Arg	Leu				
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His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser				
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Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln				
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Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	Val	Ala				
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Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly				
	610					615					620								
Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	His	Thr				
625					630					635					640				
Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	Pro				
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Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	Gly				
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Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu				
		675					680					685							
Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg				
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Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr	Val				
705					710					715					720				
Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg				
				725					730					735					

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
740 745 750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
755 760 765

Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala  
770 775 780

Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala  
785 790 795 800

Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro  
805 810 815

Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly  
820 825 830

His His His His His His  
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<210> 477

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 477

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tggc

64

<210> 478

<211> 64

<212> DNA

<213> Artificial Sequence

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<400> 478  
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<210> 479

<211> 41

<212> DNA

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<210> 480

<211> 42

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<400> 480  
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<210> 481

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gaaccggtgc aggcggtcta cggtctcgcc aagagcctcc tcaaggccct gaaggaggac 180

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<210> 482

<211> 1045

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 482

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Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu
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Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
           35                  40                  45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
       50                  55                  60

Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
   65                  70                  75                  80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
           85                  90                  95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
          100                 105                 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
      115                 120                 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
      130                 135                 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
   145                 150                 155                 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
          165                 170                 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
          180                 185                 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
      195                 200                 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
      210                 215                 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
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Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
          245                 250                 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
          260                 265                 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
      275                 280                 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
290 295 300  
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
305 310 315 320  
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
325 330 335  
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
340 345 350  
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
355 360 365  
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
370 375 380  
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
385 390 395 400  
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
405 410 415  
His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
420 425 430  
Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
435 440 445  
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
450 455 460  
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
465 470 475 480  
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
485 490 495  
Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
500 505 510  
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
515 520 525  
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys

530		535		540
Leu 545	Lys	Asn	Thr	Tyr
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			Leu	Pro
			Ser 555	Leu
			Val	His
			Pro	Arg 560
Thr	Gly	Arg	Leu	His
		565	Thr	Arg
			Phe	Asn
			Gln 570	Thr
			Ala	Thr
			Ala	Thr
			575	Gly
Arg	Leu	Ser	Ser	Ser
		580	Asp	Pro
			Asn	Leu
			Gln 585	Asn
			Ile	Pro
			Val	Arg
			590	Thr
Pro	Leu	Gly	Gln	Arg
		595	Ile	Arg
			Arg	Ala
			600	Phe
			Val	Ala
			605	Glu
			Ala	Gly
			Trp	
Ala	Leu	Val	Ala	Leu
		610	Asp	Tyr
			615	Ser
			Gln	Ile
			Glu	Leu
			620	Arg
			Val	Leu
			Ala	
His	Leu	Ser	Gly	Asp
			630	Glu
			Asn	Leu
			Ile	Arg
			Val	Phe
			635	Gln
			Glu	Gly
			Lys	640
Asp	Ile	His	Thr	Gln
			645	Thr
			Ala	Ser
			Trp	Met
			650	Phe
			Gly	Val
			Pro	Pro
			655	Glu
Ala	Val	Asp	Pro	Leu
		660	Met	Arg
			Arg	Ala
			665	Ala
			Lys	Thr
			Val	Asn
			670	Phe
			Gly	
Val	Leu	Tyr	Gly	Met
		675	Ser	Ala
			His	Arg
			680	Leu
			Ser	Gln
			685	Glu
			Leu	Ala
			Ile	
Pro	Tyr	Glu	Glu	Ala
		690	Val	Ala
			695	Phe
			Ile	Glu
			Arg	Tyr
			700	Phe
			Gln	Ser
			Phe	
Pro	Lys	Val	Arg	Ala
			710	Trp
			Ile	Glu
			Lys	Thr
			715	Leu
			Glu	Glu
			Gly	Arg
			Lys	720
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			Leu	Phe
			Gly	Arg
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			Arg	Tyr
			Val	Pro
			735	Asp
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			745	Glu
			Ala	Ala
			Glu	Arg
			750	Met
			Ala	
Phe	Asn	Met	Pro	Val
		755	Gln	Gly
			Thr	Ala
			760	Ala
			Asp	Leu
			765	Met
			Lys	Leu
			Ala	
Met	Val	Lys	Leu	Phe
			770	Pro
			Arg	Leu
			775	Arg
			Glu	Met
			780	Gly
			Ala	Arg
			Met	Leu

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830

Ser Ala Lys Gly His His His His His His Val Asp Met Thr Met Ile  
 835 840 845

Thr Pro Ser Tyr Leu Gly Asp Thr Ile Glu Tyr Ser Ser Tyr Ala Ser  
 850 855 860

Ser Leu Val Pro Ser Ser Asp Pro Leu Val Thr Ala Ala Ser Val Leu  
 865 870 875 880

Glu Phe Cys Arg Tyr Pro Ser His Trp Arg Pro Leu Glu His Ala Ser  
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Arg Gly Pro Asn Ser Pro Tyr Ser Glu Ser Tyr Tyr Asn Ser Leu Ala  
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Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu  
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Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu  
 930 935 940

Glu Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly  
 945 950 955 960

Glu Trp Asp Ala Pro Cys Ser Gly Ala Leu Ser Ala Ala Gly Val Val  
 965 970 975

Val Thr Arg Ser Val Thr Ala Thr Leu Ala Ser Ala Leu Ala Pro Ala  
 980 985 990

Pro Phe Ala Phe Phe Pro Ser Phe Leu Ala Thr Phe Ala Gly Phe Pro  
 995 1000 1005

Arg Gln Ala Leu Asn Arg Gly Leu Pro Leu Gly Phe Arg Phe Arg  
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Ser Arg Ser Gly Pro Ser Pro  
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<211> 36.

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

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ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggcctcaa ggaggacggg	180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg	240
gggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc	300
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag	480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg	540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcac	600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag	660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg	720



aagctctcct	gggacctggc	caaggtgcgc	accgacctgc	ccctggaggt	ggacttcgcc	780
aaaaggcggg	agccccgaccg	ggagaggctt	agggcctttc	tggagaggct	tgagtttgcc	840
agcctcctcc	acgagttcgg	ccttctggaa	agcccccaagg	ccctggagga	ggccccctgg	900
cccccgccgg	aaggggcctt	cgtgggcttt	gtgctttccc	gcaaggagcc	catgtgggcc	960
gatcttctgg	ccctggccgc	cgccaggggc	ggccgcgtgc	accgggcagc	agacccttg	1020
gcggggctaa	aggacctcaa	ggaggtccgg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
gcctcgaggg	aggggctaga	cctcgtgccc	ggggacgacc	ccatgctcct	cgccctacctc	1140
ctggaccctt	cgaacaccac	ccccgagggg	gtggcgcggc	gctacggggg	ggagtggacg	1200
gaggacgccg	cccaccgggc	cctcctctcg	gagaggctcc	atcggaacct	ccttaagcgc	1260
ctcgaggggg	aggagaagct	cctttggctc	taccacgagg	tggaaaagcc	cctctcccgg	1320
gtcctggccc	atatggaggc	caccggggta	cgccgggacg	tggcctacct	tcaggccctt	1380
tccctggagc	ttgcggagga	gatccgccgc	ctcgaggagg	aggtcttccg	cttggcgggc	1440
caccccttca	acctcaactc	ccgggaccag	ctggaaaggg	tgctctttga	cgagcttagg	1500
cttccgcct	tgaagaagac	gaagaagaca	ggcaagcgct	ccaccagcgc	cgcggtgctg	1560
gaggccctac	gggaggccca	ccccatcgtg	gagaagatcc	tccagcaccg	ggagctcacc	1620
aagctcaaga	acacctacgt	ggacccccctc	ccaagcctcg	tccacccgag	gacgggcccgc	1680
ctccacaccc	gcttcaacca	gacggccacg	gccacgggga	ggcttagtag	ctccgacccc	1740
aacctgcaga	acatccccgt	ccgcaccccc	ttggggccaga	ggatccgccg	ggccttcgtg	1800
gccgaggcgg	gttgggcgtt	ggtggccctg	gactatagcc	agatagagct	ccgcgtcctc	1860
gcccacctct	ccggggacga	aaacctgata	agggctcttc	aggaggggaa	ggacatccac	1920
accagaccg	caagctggat	gttcggcgtc	cccccgagg	ccgtggaccc	cctgatgcgc	1980
cgggcggcca	agacggtgaa	cttcggcgtc	ctctacggca	tgtccgcca	taggctctcc	2040
caggagcttg	ccatccccta	cgaggaggcg	gtggccttta	tagagcgcta	cttccaaagc	2100
ttccccaaag	tgcgggcctg	gatagaaaag	accctggagg	aggggaggaa	gcggggctac	2160
gtggaaaccc	tcttcggaag	aaggcgctac	gtgcccgaac	tcaacgcccg	ggtgaagagc	2220
gtcagggagg	ccgcggagcg	catggccttc	aacatgcccg	tccagggcac	cgccgccgac	2280
ctcatgaagc	tcgccatggt	gaagctcttc	ccccgcctcc	gggagatggg	ggccccgatg	2340
ctcctccagg	tcgccaacga	gctcctcctg	gaggcccccc	aagcgcgggc	cgaggaggtg	2400
gcggcttttg	ccaaggaggc	catggagaag	gcctatcccc	tcgccgtgcc	cctggaggtg	2460
gaggtgggga	tgggggagga	ctggctttcc	gccaagggtc	accaccacca	ccaccac	2517

<210> 485

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 485

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400

Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430

Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
450 455 460

Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
485 490 495

Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
515 520 525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
530 535 540

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His  
625 630 635 640

Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
675 680 685

Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val

690	695	700
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr 705 710 715 720		
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala 725 730 735		
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met 740 745 750		
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys 755 760 765		
Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val 770 775 780		
Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val 785 790 795 800		
Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val 805 810 815		
Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys 820 825 830		
Gly His His His His His His 835		

<210> 486

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 486

gtggaccttc tgggctttac ccgcctcgag gccccg

36

<210> 487

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 487  
cggggcctcg aggcgggtaa agcccagaag gtccac

36

<210> 488

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 488

Met Asn Ser Thr Pro Leu Phe Asp Leu Glu Glu Pro Pro Lys Arg Val  
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Tyr Ala Leu  
20 25 30

Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe  
35 40 45

Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
100 105 110

Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys  
115 120 125

Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg  
130 135 140

Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp  
 145 150 155 160

Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro  
 165 170 175

Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp  
 180 185 190

Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu  
 195 200 205

Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg  
 210 215 220

Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp  
 225 230 235 240

Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu  
 245 250 255

Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly  
 260 265 270

Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285

Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro  
 290 295 300

Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro  
 305 310 315 320

Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val  
 325 330 335

His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350

Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380

Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly

385		390		395		400
Glu Trp Thr	Glu Asp	Ala Ala His Arg	Ala Leu Leu Ser	Glu Arg	Leu	
	405		410	415		
His Arg Asn	Leu Leu Lys Arg	Leu Glu Gly	Glu Glu Lys	Leu Leu Trp		
	420	425	430			
Leu Tyr His	Glu Val Glu Lys	Pro Leu Ser Arg	Val Leu Ala His	Met		
	435	440	445			
Glu Ala Thr	Gly Val Arg Arg	Asp Val Ala Tyr	Leu Gln Ala	Leu Ser		
	450	455	460			
Leu Glu Leu	Ala Glu Glu Ile Arg	Arg Leu Glu Glu Glu	Val Phe Arg			
465	470	475	480			
Leu Ala Gly	His Pro Phe Asn	Leu Asn Ser Arg	Asp Gln Leu Glu	Arg		
	485	490	495			
Val Leu Phe	Asp Glu Leu Arg	Leu Pro Ala Leu Lys	Lys Thr Lys Lys			
	500	505	510			
Thr Gly Lys	Arg Ser Thr Ser	Ala Ala Val Leu Glu	Ala Leu Arg Glu			
	515	520	525			
Ala His Pro	Ile Val Glu Lys Ile	Leu Gln His Arg	Glu Leu Thr Lys			
	530	535	540			
Leu Lys Asn	Thr Tyr Val Asp	Pro Leu Pro Ser	Leu Val His Pro	Arg		
545	550	555	560			
Thr Gly Arg	Leu His Thr Arg	Phe Asn Gln Thr	Ala Thr Ala Thr	Gly		
	565	570	575			
Arg Leu Ser	Ser Ser Asp Pro	Asn Leu Gln Asn Ile	Pro Val Arg Thr			
	580	585	590			
Pro Leu Gly	Gln Arg Ile Arg	Arg Ala Phe Val	Ala Glu Ala Gly	Trp		
	595	600	605			
Ala Leu Val	Ala Leu Asp Tyr	Ser Gln Ile Glu	Leu Arg Val Leu	Ala		
	610	615	620			
His Leu Ser	Gly Asp Glu Asn	Leu Ile Arg Val	Phe Gln Glu Gly	Lys		
625	630	635	640			



Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
820 825 830

Ser Ala Lys Gly His His His His His His  
835 840

<210> 489

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 489

tttaccgcgcc tcgagggtgcc gggc

24

<210> 490

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 490

cggcacctcg aggcgggtaa agcccaaaag gtccac

36

<210> 491

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 491

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val  
1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu  
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys  
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val  
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr  
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
 85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val  
 100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala  
 115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu  
 130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr  
 145 150 155 160

Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser  
 165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile  
 180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg  
 195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys  
 210 215 220

Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys  
 225 230 235 240

Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val  
 245 250 255

Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe  
 260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285

Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300

Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
 305 310 315 320

Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala  
 325 330 335

Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu  
340 345 350

Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val  
355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
370 375 380

Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
385 390 395 400

Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu  
405 410 415

Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu  
420 425 430

Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
435 440 445

Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala  
450 455 460

Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His  
465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
485 490 495

Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg  
500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
515 520 525

Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr  
530 535 540

Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu  
545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
565 570 575

Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln

580										585					590				
Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	Val	Ala				
		595					600					605							
Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly				
	610					615					620								
Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	His	Thr				
625					630					635					640				
Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	Pro				
				645					650					655					
Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	Gly				
			660					665					670						
Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu				
		675					680					685							
Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg				
	690					695					700								
Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr	Val				
705					710					715					720				
Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg				
				725					730					735					
Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro				
			740					745					750						
Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu				
		755					760					765							
Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	Ala				
	770					775					780								
Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val	Ala				
785					790					795					800				
Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val	Pro				
				805					810					815					
Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Gly				
		820						825					830						

His His His His His His  
835

<210> 492

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 492

atcgtggtct ttgacgccga ggccccctcc ttcc

34

<210> 493

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 493

ggaaggaggg ggcctcggcg tcaaagacca cgat

34

<210> 494

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 494

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60

Val Phe Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110

Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140

Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160

Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190

Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
195 200 205

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
210 215 220

Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
225 230 235 240

Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
260 265 270

Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu

275					280					285					
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro
290						295					300				
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro
305					310					315					320
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Gly	Gly	Arg	Val
				325					330					335	
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val
			340					345					350		
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly
		355					360					365			
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu
	370					375					380				
Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly
385					390					395					400
Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu
				405					410					415	
His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp
			420					425					430		
Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met
		435					440					445			
Glu	Ala	Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser
	450					455					460				
Leu	Glu	Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg
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Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg
				485					490					495	
Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys
			500					505					510		
Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu
		515					520					525			



Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830

Ser Ala Lys Gly His His His His His His  
 835 840

<210> 495

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 495

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ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg	180
gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg	240
gggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgccctcatc	300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatactc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccacccccgag	480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg	540
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<210> 496

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 496

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
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Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190 \

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365  
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
 450 455 460  
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly

465		470		475		480									
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe
			485					490						495	
Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys
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Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro
		515					520					525			
Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn
	530					535					540				
Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	Arg
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Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser
				565					570					575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly
			580					585					590		
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	Val
		595					600					605			
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser
	610					615					620				
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	His
625					630					635					640
Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp
				645					650					655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr
			660					665					670		
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu
		675					680					685			
Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val
	690					695					700				
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr
705					710					715					720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala  
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
755 760 765

Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
770 775 780

Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val  
785 790 795 800

Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Gly His His His His His His  
835

<210> 497

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 497

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ccggtgcaga tgggtctacgg cttcgcccgg agcctcctca aggccttgaa ggaggacgga      180
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gacgtcctgg gcaccctggc caagaaggcc gaaagggagg ggatggaggt gcgcatectc      420
acgggagacc gggacttctt ccagctcctc tccgagaagg tctcggtcct cctgccggac      480
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<210> 498

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 498

Met Asn Ser Thr Pro Leu Phe Asp Leu Glu Glu Pro Pro Lys Arg Val  
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 20 25 30

Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe  
 35 40 45

Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val  
 50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
 65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95

Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg Leu  
 100 105 110

Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys  
 115 120 125

Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg  
 130 135 140

Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp

145		150		155		160
Gly Thr Leu Val Thr	Pro Lys Asp Val	Gln Glu Lys Tyr Gly	Val Pro			
	165	170	175			
Pro Glu Arg Trp Val	Asp Phe Arg Ala	Leu Thr Gly Asp	Arg Ser Asp			
	180	185	190			
Asn Ile Pro Gly Val	Ala Gly Ile Gly	Glu Lys Thr Ala	Leu Arg Leu			
	195	200	205			
Leu Ala Glu Trp Gly	Ser Val Glu Asn	Leu Leu Lys Asn	Leu Asp Arg			
	210	215	220			
Val Lys Pro Asp Ser	Leu Arg Arg Lys	Ile Glu Ala His	Leu Glu Asp			
	225	230	235			240
Leu His Leu Ser	Leu Asp Leu Ala	Arg Ile Arg Thr	Asp Leu Pro	Leu		
	245	250	255			
Glu Val Asp Phe Lys	Ala Leu Arg Arg	Arg Thr Pro Asp	Leu Glu Gly			
	260	265	270			
Leu Arg Ala Phe Leu	Glu Glu Leu Glu	Phe Gly Ser Leu	Leu His Glu			
	275	280	285			
Phe Gly Leu Leu Gly	Gly Glu Lys Pro	Arg Glu Glu Ala	Pro Trp Pro			
	290	295	300			
Pro Pro Glu Gly Ala	Phe Val Gly Phe	Leu Leu Ser Arg	Lys Glu Pro			
	305	310	315			320
Met Trp Ala Glu Leu	Leu Ala Leu Ala	Ala Ala Ser Gly	Gly Arg Val			
	325	330	335			
His Arg Ala Ala Asp	Pro Leu Ala Gly	Leu Lys Asp Leu	Lys Glu Val			
	340	345	350			
Arg Gly Leu Leu Ala	Lys Asp Leu Ala	Val Leu Ala Ser	Arg Glu Gly			
	355	360	365			
Leu Asp Leu Val Pro	Gly Asp Asp Pro	Met Leu Leu Ala	Tyr Leu Leu			
	370	375	380			
Asp Pro Ser Asn Thr	Thr Pro Glu Gly	Val Ala Arg Arg	Tyr Gly Gly			
	385	390	395			400

Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
660 665 670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
675 680 685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
705 710 715 720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
820 825 830

Ser Ala Lys Gly His His His His His His  
835 840

<210> 499

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 499

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caggcgggtgt	acgggtttgc	caagagcctt	ttgaaggcgc	taagggaaga	cggggatgtg	180
gtgatcgtgg	tctttgacgc	cgaggccccc	tccttcgcgc	accagacctt	cgaggcctac	240
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<210> 500

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 500

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val  
 1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu  
 20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys  
 35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val  
 50 55 60

Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr  
 65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
 85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val  
 100 105 110  
 Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala  
 115 120 125  
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu  
 130 135 140  
 Tyr Gln Leu Leu Ser Glu Arg Ile Ser Ile Leu His Pro Glu Gly Tyr  
 145 150 155 160  
 Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Lys Pro Ser  
 165 170 175  
 Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile  
 180 185 190  
 Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys Leu Ile Arg  
 195 200 205  
 Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu Glu Gln Val Lys  
 210 215 220  
 Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys  
 225 230 235 240  
 Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val  
 245 250 255  
 Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe  
 260 265 270  
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285  
 Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300  
 Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
 305 310 315 320  
 Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala  
 325 330 335  
 Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu  
 340 345 350

Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu  
 405 410 415  
 Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu  
 420 425 430  
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala  
 450 455 460  
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His  
 465 470 475 480  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
 485 490 495  
 Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg  
 500 505 510  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr  
 530 535 540  
 Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu  
 545 550 555 560  
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590  
 Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala



595					600					605					
Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly
610						615					620				
Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	His	Thr
625					630					635					640
Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	Pro
				645					650					655	
Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	Gly
			660					665					670		
Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu
		675					680					685			
Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg
	690					695					700				
Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr	Val
705					710					715					720
Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg
				725					730					735	
Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro
			740					745					750		
Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu
		755					760					765			
Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	Ala
	770					775					780				
Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val	Ala
785					790					795					800
Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val	Pro
				805					810					815	
Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Gly
			820					825					830		
His	His	His	His	His	His										
		835													

<210> 501

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 501

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ccggtgcagg	cggtctacgg	cttcgccaag	agcctcctca	aggccctcaa	ggaggacggg	180
gacgcggtga	tcgtggtctt	tgacgccgag	gccccctcct	tccgccacga	ggcctacggg	240
gggtacaagg	cgggccgggc	ccccacgccg	gaggactttc	cccggcaact	cgccctcatc	300
aaggagctgg	tggacctcct	ggggttcacg	cgctcagagg	tcccgggcta	cgaggcggac	360
gacgtcctgg	ccagcctggc	caagaaggcg	gaaaaggagg	gctacgaggt	ccgcatcctc	420
accgccgaca	aagaccttta	ccagctcctt	tccgaccgca	tccacgtcct	ccaccccgag	480
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gccgactacc	gggccctgac	cggggacgag	tccgacaacc	ttcccggggg	caagggcata	600
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caccctttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500  
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<210> 502

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 502

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
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Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe

35					40					45					
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
50						55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
				165					170					175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
				245					250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400

Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430

Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
 450 455 460

Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495

Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
 530 535 540

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His  
625 630 635 640

Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
675 680 685

Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr  
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala  
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
755 760 765

Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
770 775 780

Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val

785 790 795 800

Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Gly His His His His His His  
835

<210> 503

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 503

atcgtgggtct ttgacgccga ggccccctcc ttcc

34

<210> 504

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 504

ggaaggaggg ggcctcggcg tcaaagacca cgat

34

<210> 505

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 505

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gagccggtgc	aggcggtcta	cggcttcgcc	aagagcctcc	tcaaggccct	caaggaggac	180
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gggggggtaca	aggcgggccc	ggccccacg	ccggaggact	ttccccggca	actcgccctc	300
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gacgacgtcc	tggccagcct	ggccaagaag	gcggaaaagg	agggctacga	ggtccgcatac	420
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gaggggtacc	tcatcacccc	ggcctggctt	tgggaaaagt	acggcctgag	gcccgaccag	540
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atcggggaga	agacggcgag	gaagcttctg	gaggagtggg	ggagcctgga	agccctcctc	660
aagaacctgg	accggctgaa	gcccgccatc	cgggagaaga	tcctggccca	catggacgat	720
ctgaagctct	cctgggacct	ggccaagggt	cgcaccgacc	tgccccctgga	ggtggacttc	780
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gccgatcttc	tggccctggc	cgccgccagg	ggcgcccgcg	tgcaccgggc	agcagacccc	1020
ttggcggggc	taaaggacct	caaggagggt	cggggcctcc	tcgccaagga	cctcgccgtc	1080
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acggaggacg	ccgcccaccg	ggccctcctc	tcggagaggc	tccatcgga	cctccttaag	1260
cgcctcgagg	gggaggagaa	gctccttttg	ctctaccacg	aggtggaaaa	gcccctctcc	1320
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ctttccctgg	agcttgcgga	ggagatccgc	cgcctcgagg	aggaggctct	ccgcttggcg	1440
ggccacccct	tcaacctcaa	ctcccgggac	cagctggaaa	gggtgctctt	tgacgagctt	1500
aggcttcccc	ccttgaagaa	gacgaagaag	acaggcaagc	gctccaccag	cgccgcggtg	1560
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accaagctca	agaacaccta	cgtggacccc	ctcccaagcc	tcgtccaccc	gaggacgggc	1680
cgcctccaca	cccgttcaa	ccagacggcc	acggccacgg	ggaggcttag	tagctccgac	1740
cccaacctgc	agaacatccc	cgtccgcacc	cccttggggc	agaggatccg	ccgggccttc	1800



gtggccgagg cgggttgggc gttggtggcc ctggactata gccagataga gctccgcgtc 1860  
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cacaccaga ccgcaagctg gatgttcggc gtcccccccg aggccgtgga cccctgatg 1980  
cgccggggcgg ccaagacggt gaacttcggc gtcctctacg gcatgtccgc ccataggctc 2040  
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agcgtcaggg aggccgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc 2280  
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gtggcggcct tggccaagga ggccatggag aaggcctatc ccctcgccgt gccctggag 2460  
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<210> 506

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 506

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val  
50 55 60

Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr  
65 70 75 80

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg

- 784 -

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly  
 340 345 350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp  
 355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
 405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
 435 440 445

Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
 450 455 460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala  
 465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly  
 500 505 510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His  
 515 520 525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys  
 530 535 540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly  
 545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
 565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
 580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu  
 595 600 605  
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
 610 615 620  
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile  
 625 630 635 640  
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val  
 645 650 655  
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670  
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
 675 680 685  
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
 690 695 700  
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly  
 705 710 715 720  
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn  
 725 730 735  
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
 740 745 750  
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val  
 755 760 765  
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln  
 770 775 780  
 Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu  
 785 790 795 800  
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala  
 805 810 815  
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala  
 820 825 830  
 Lys Gly His His His His His His

835

840

&lt;210&gt; 507

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic

&lt;400&gt; 507

cagaccatga attcggaggc gatgctgcc ctcttt

36

&lt;210&gt; 508

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic

&lt;400&gt; 508

aaagaggggc agcatcgct ccgaattcat ggtctg

36

&lt;210&gt; 509

&lt;211&gt; 2517

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic

&lt;400&gt; 509

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60

caccacctgg cctaccgcac cttctttgcc ctgaagggcc tcaccaccag ccgggggggag

120

ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg

180

gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg

240

gggtacaagg	cgggccgggc	ccccacgccg	gaggactttc	cccggcaact	cgccctcatc	300
aaggagctgg	tggacctcct	ggggttcacg	cgctcgagg	tcccgggcta	cgaggcggac	360
gacgtcctgg	ccagcctggc	caagaaggcg	gaaaaggagg	gctacgaggt	ccgcatcctc	420
accgccgaca	aagaccttta	ccagctcctt	tccgaccgca	tccacgtcct	ccaccccag	480
gggtacctca	tcaccccggc	ctggctttgg	gaaaagtacg	gcctgaggcc	cgaccagtgg	540
gccgactacc	gggccctgac	cggggacgag	tccgacaacc	ttcccggggt	caagggcatc	600
ggggagaaga	cggcgaggaa	gcttctggag	gagtggggga	gcctggaagc	cctcctcaag	660
aacctggacc	ggctgaagcc	cgccatccgg	gagaagatcc	tggcccacat	ggacgatctg	720
aagctctcct	gggacctggc	caagggtgcg	accgacctgc	ccctggaggt	ggacttcgcc	780
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gcggggctaa	aggacctcaa	ggaggtccgg	ggcctcctcg	ccaaggacct	cgccgtcttg	1080
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cttccgcct	tgaagaagac	gaagaagaca	ggcaagcgct	ccaccagcgc	cgcggtgctg	1560
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gccgaggcgg	gttgggcgtt	ggtggccctg	gactatagcc	agatagagct	ccgcgtcctc	1860
gcccacctct	ccggggacga	aaacctgatc	agggctcttc	aggaggggaa	ggacatccac	1920
accagaccg	caagctggat	gttcggcgtc	ccccggagg	ccgtggaccc	cctgatgcgc	1980
cgggcggcca	agacggtgaa	cttcggcgtc	ctctacggca	tgtccgcca	taggctctcc	2040
caggagcttg	ccatccccta	cgaggaggcg	gtggccttta	tagagcgcta	cttccaaagc	2100

ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160  
 gtggaaaccc tcttcggaag aaggcgctac gtgcccgacc tcaacgcccg ggtgaagagc 2220  
 gtcagggagg ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tcgccatggt gaagctcttc cccgcctcc gggagatggg ggcccgcacg 2340  
 ctctccagg tcgccaacga gctcctcctg gagggccccc aagcgcgggc cgaggaggtg 2400  
 gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460  
 gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 510

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 510

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
 1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys  
 20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
 100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380



Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
 450 455 460  
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
 530 535 540  
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His

625		630		635		640									
Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp
				645					650					655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr
			660					665					670		
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu
		675					680					685			
Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val
	690					695					700				
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr
705					710					715					720
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala
				725					730					735	
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met
			740					745					750		
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys
		755					760					765			
Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val
	770					775					780				
Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val
785					790					795					800
Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val
				805					810					815	
Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys
			820					825					830		
Gly	His	His	His	His	His	His	His								
		835													

<210> 511

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 511

gcctaccgca ccttctttgc cctgaagggc etc

33

<210> 512

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 512

gaggcccttc agggcaaaga aggtgcggta ggc

33

<210> 513

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 513

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caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120

ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcag agaggacggg 180

gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg 240

gggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgccctcatc 300

aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360

gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatactc 420

accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480

gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540

gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcac 600

ggggagaaga	cggcgaggaa	gcttctggag	gagtggggga	gcctggaagc	cctcctcaag	660
aacctggacc	ggctgaagcc	cgccatccgg	gagaagatcc	tggcccacat	ggacgatctg	720
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aaaaggcggg	agccccgaccg	ggagaggctt	agggcctttc	tggagaggct	tgagtttggc	840
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gcggccttgg	ccaaggaggc	catggagaag	gcctatcccc	tcgccgtgcc	cctggagggtg	2460

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<210> 514

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 514

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400

Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430

Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
450 455 460

Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
485 490 495

Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
515 520 525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
530 535 540

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His  
625 630 635 640

Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu

675		680		685											
Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val
690						695					700				
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr
705					710					715					720
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala
				725					730					735	
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met
			740					745					750		
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys
		755					760					765			
Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val
	770					775					780				
Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val
785					790				795						800
Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val
				805					810					815	
Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys
			820					825					830		
Gly	His	His	His	His	His	His									
	835														

<210> 515

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 515

ctcctcaagg ccctcagaga ggacggggac gcg

33

<210> 516



<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 516

cgcgccccg tcctctctga gggccttgag gag

33

<210> 517

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 517

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc	60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag	120
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg	180
gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggccctacggg	240
gggtacaagg cgggcccggc cccacgccc gaggactttc cccggcaact cgccctcatc	300
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccacctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatactc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccacccccgag	480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg	540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc	600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag	660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg	720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc	780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc	840
agcctcctcc acgagttcgg ctttctggaa agccccaagg ccctggagga ggccccctgg	900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc	960

gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agaccccttg	1020
gcgggggctaa aggacctcaa ggaggtccgg ggctcctcgc ccaaggacct cgccgtcttg	1080
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgctacctc	1140
ctggaccctt cgaacaccac ccccagggg gtggcgcggc gctacggggg ggagtggacg	1200
gaggacgccg ccacccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc	1260
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg	1320
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt	1380
tccctggagc ttgcggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc	1440
caccccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg	1500
cttccgcct tgaagaagac gaagaagaca ggcaagcgct ccaccagcgc cgcggtgctg	1560
gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc	1620
aagctcaaga acacctacgt ggacccctc ccaagcctcg tccacccgag gacgggccgc	1680
ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc	1740
aacctgcaga acatccccgt ccgcaccccc ttggggcaga ggatccgccg ggcttcgtg	1800
gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc	1860
gcccacctct ccggggacga aaacctgatc agggctcttc aggaggggaa ggacatccac	1920
accagaccg caagctggat gttcggcgtc ccccgaggg ccgtggacc cctgatgcgc	1980
cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc	2040
caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc	2100
ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac	2160
gtggaaaccc tcttcggaag aaggcgctac gtgcccgacc tcaacgccc ggtgaagagc	2220
gtcagggagg ccgcggagcg catggccttc aacatgccc tccagggcac cgccgccgac	2280
ctcatgaagc tcgccatggt gaagctcttc cccgcctcc gggagatggg ggcccgcag	2340
ctcctccagg tcgccaacga gctcctcctg gaggcccccc aagcgcgggc cgaggaggtg	2400
gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg	2460
gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac	2517

<210> 518

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 518

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365  
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
 450 455 460  
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
 530 535 540  
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His  
 625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala



<400> 520  
cgccttcttg gccaggggtg ccaggacgtc gtc

33

<210> 521

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 521

atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc	60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag	120
ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg	180
gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg	240
gggtacaagg cgggccgggc cccacacgcc gaggactttc cccggcaact cgccctcatc	300
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatactc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag	480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg	540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatac	600
ggggagaaga cggcgctcaa gcttctggag gagtggggga gcctggaagc cctcctcaag	660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg	720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggagggt ggacttcgcc	780
aaaaggcggg agcccgaccg ggagaggcct agggcctttc tggagaggct tgagtttggc	840
agcctcctcc acgagttcgg ccttctggaa agccccaagg ccctggagga ggccccctgg	900
cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc	960
gatcttcttg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg	1020
gcggggctaa aggacctcaa ggaggtccgg ggcctcctcg ccaaggacct cgccgtcttg	1080
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc	1140
ctggacctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg	1200
gaggacgccg cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc	1260
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg	1320

gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380  
tccctggagc ttgcggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc 1440  
cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500  
cttcccgct tgaagaagac gaagaagaca ggcaagcgct ccaccagcgc cgcggtgctg 1560  
gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620  
aagctcaaga acacctacgt ggacccccctc ccaagcctcg tccacccgag gacgggccgc 1680  
ctccacaccc gcttcaacca gacggccaacg gccacgggga ggcttagtag ctccgacccc 1740  
aacctgcaga acatccccgt ccgcaccccc ttggggcaga ggatccgccg ggccttcgtg 1800  
gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc 1860  
gcccacctct ccggggacga aaacctgatc agggctcttc aggaggggaa ggacatccac 1920  
accagaccg caagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980  
cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc 2040  
caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100  
ttcccaaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160  
gtggaaaccc tcttcggaag aaggcgctac gtgcccgacc tcaacgcccg ggtgaagagc 2220  
gtcagggagg ccgcggagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
ctcatgaagc tcgccatggt gaagctcttc ccccgctcc gggagatggg ggcccgcgatg 2340  
ctctccagg tcgccaacga gtcctcctg gagggccccc aagcgcgggc cgaggagggtg 2400  
gcggttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggagggtg 2460  
gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 522

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 522

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys



20	25	30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe		
35	40	45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile		
50	55	60
Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly		
65	70	75
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln		
85	90	95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu		
100	105	110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys		
115	120	125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys		
130	135	140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu		
145	150	155
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg		
165	170	175
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp		
180	185	190
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu		
195	200	205
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg		
210	215	220
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu		
225	230	235
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu		
245	250	255
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala		
260	265	270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
275 280 285  
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
290 295 300  
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
305 310 315 320  
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
325 330 335  
Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
340 345 350  
Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
355 360 365  
Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
370 375 380  
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
385 390 395 400  
Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
405 410 415  
Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
420 425 430  
Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
435 440 445  
Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
450 455 460  
Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
465 470 475 480  
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
485 490 495  
Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
500 505 510  
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
515 520 525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
 530 535 540

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
 595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His  
 625 630 635 640

Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
 660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685

Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr  
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala  
 725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765

Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val

770		775		780
Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val				
785		790	795	800
Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val				
	805		810	815
Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys				
	820	825	830	
Gly His His His His His His				
	835			

<210> 523

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 523

ggggagaaga cggcgctcaa gcttctggag gag

33

<210> 524

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 524

ctcctccaga agcttgagcg ccgtcttctc ccc

33

<210> 525

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 525

atgaattcgg	ggatgctgcc	cctctttgag	cccaagggcc	gggtcctcct	ggtggacggc	60
caccacctgg	cctaccgcac	cttcacgcc	ctgaagggcc	tcaccaccag	ccggggggag	120
ccggtgcagg	cggtctacgg	cttcgccaag	agcctcctca	aggccctcaa	ggaggacggg	180
gacgcggtga	tcgtggtctt	tgacgccgag	gccccctcct	tccgccacga	ggcctacggg	240
gggtacaagg	cgggccgggc	ccccacgccg	gaggactttc	cccggcaact	cgccctcatc	300
aaggagctgg	tggacctcct	ggggttcacg	cgctcagagg	tcccgggcta	cgaggcggac	360
gacgtcctgg	ccagcctggc	caagaaggcg	gaaaaggagg	gctacgaggt	ccgcatactc	420
accgccgaca	aagaccttta	ccagctcctt	tccgaccgca	tccacgtcct	ccaccccgag	480
gggtacctca	tcaccccggc	ctggcttttg	gaaaagtacg	gcctgaggcc	cgaccagtgg	540
gccgactacc	gggccctgac	cggggacgag	tccgacaacc	ttcccggggg	caagggcatc	600
ggggagaaga	cggcgaggaa	gcttctggag	gagtggggga	gcctggaagc	cctcctcaag	660
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Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
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Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly

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Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
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Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
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Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
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Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala
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Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
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Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
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Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
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Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
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Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
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Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
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Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
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His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
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Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
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Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
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Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
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Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
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Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
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Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
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Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
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Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His  
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Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
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Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
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Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
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Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
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Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr  
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Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala  
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Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
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Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
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Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val  
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Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val  
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Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys

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Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
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Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
 100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
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Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285

Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
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Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
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Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
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Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
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Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
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Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
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Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
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His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
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Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
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Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
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Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
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Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
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Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
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Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
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Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser

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Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys
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ctccacaccc	gcttcaacca	gacggccacg	gccacgggga	ggcttagtag	ctccgacccc	1740
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gccgaggcgg	gttgggcgtt	ggtggccctg	gactatagcc	agatagagct	ccgcgtcctc	1860
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accagaccg	caagctggat	gttcggcgtc	cccccgagg	ccgtggaccc	cctgatgcgc	1980
cgggcggcca	agacggtgaa	cttcggcgtc	ctctacggca	tgtccgcca	taggctctcc	2040
caggagcttg	ccatccccta	cgaggaggcg	gtggccttta	tagagcgcta	cttccaaagc	2100
ttccccaagg	tgcgggcctg	gatagaaaag	accctggagg	aggggaggaa	gcggggctac	2160
gtggaaaccc	tcttcggaag	aaggcgctac	gtgcccgacc	tcaacgcccg	ggtgaagagc	2220
gtcagggagg	ccgcggagcg	catggccttc	aacatgcccg	tccagggcac	cgccgccgac	2280
ctcatgaagc	tcgcatgggt	gaagctcttc	ccccgcctcc	gggagatggg	ggccccgatg	2340

ctcctccagg tcgccaacga gctcctcctg gaggcccccc aagcgcgggc cgaggaggtg 2400  
gcggtctttgg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460  
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<210> 534

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 534

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg Ala  
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400

Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430

Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
 450 455 460

Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495

Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525

Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
 530 535 540

Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590

Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
 595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His  
 625 630 635 640

Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr

	660		665		670														
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu				
	675						680					685							
Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val				
	690					695					700								
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr				
705					710					715					720				
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala				
				725					730					735					
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met				
			740					745					750						
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys				
		755					760					765							
Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val				
	770					775					780								
Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val				
785					790					795					800				
Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val				
				805					810					815					
Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys				
			820					825					830						
Gly	His	His	His	His	His	His													
	835																		

<210> 535

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 535

ctggccctgg ccgcctgcag gggcggccgc gtg 33

<210> 536

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 536

cacgcggccg cccctgcagg cggccagggc cag 33

<210> 537

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 537

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ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggcccggc cccacgccg gaggactttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccgggggt caagggcatc 600  
ggggagaaga cggcgaggaa gcttctgaag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
aagctctcct gggacctggc caaggcgcc accgacctgc ccctggaggt ggacttcgcc 780

aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc	840
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gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg	1020
gcggggctaa aggacctcaa ggaggtccgg ggctcctcg ccaaggacct cgccgtcttg	1080
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgccctacctc	1140
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accagaccg caagctggat gttcggcgtc ccccgaggg ccgtggacc cctgatgcgc	1980
cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc	2040
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ctcctccagg tcgccaacga gctcctcctg gaggcccccc aagcgcgggc cgaggaggtg	2400
gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggagggtg	2460
gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac	2517

<210> 538

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 538

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205



Leu Lys Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335

Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350

Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365

Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400

Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415

Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430

Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu

450		455		460
Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly				
465		470		475 480
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe				
	485		490	495
Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys				
	500		505	510
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro				
	515		520	525
Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn				
	530		535	540
Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg				
	545		550	555 560
Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser				
	565		570	575
Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly				
	580		585	590
Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val				
	595		600	605
Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser				
	610		615	620
Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His				
	625		630	635 640
Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp				
	645		650	655
Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr				
	660		665	670
Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu				
	675		680	685
Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val				
	690		695	700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr  
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala  
 725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765

Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780

Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val  
 785 790 795 800

Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val  
 805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830

Gly His His His His His His  
 835

<210> 539

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 539  
 ggggagaaga cggcgaggaa gcttctgaag gagggggga gc

42

<210> 540

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 540

gctccccac tccttcagaa gcttcctcgc cgtcttctcc cc

42

<210> 541

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 541

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gagccggtgc aggcggtcta cggtctcgcc aagagcctcc tcaaggccct cagagaggac	180
ggggacgcgg tgatcgtggt ctttgacgcc gaggccccct ccttcgcga cgaggcctac	240
gggggggtaca aggcggggccg ggccccacg ccggaggact ttccccggca actcgccctc	300
atcaaggagc tgggtggacct cctgggggtt acgcgcctcg aggtcccggg ctacgaggcg	360
gacgacgtcc tggccaccct ggccaagaag gcggaaaagg agggctacga ggtccgcatc	420
ctcaccgccc acaaagacct ttaccagctc ctttcgcacc gcatccacgt cctccacccc	480
gaggggtacc tcatcacccc ggcttggtt tgggaaaagt acggcctgag gcccgaccag	540
tgggccgact accggggcct gaccggggac gagtccgaca accttcccgg ggtcaagggc	600
atcggggaga agacggcgct caagcttctg gaggagtggg ggagcctgga agccctcctc	660
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ctgaagctct cctgggacct ggccaagggt cgcaccgacc tgcccctgga ggtggacttc	780
gccaaaaggc gggagcccga ccgggagggg cttaaggcct ttctggagag gcttgagttt	840
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tggccccgc cggaaggggc cttcgtgggc tttgtgcttt cccgcaagga gcccatgtgg	960
gccgatcttc tggccctggc cgctgcagg ggcggccgcg tgcaccgggc agcagacccc	1020
ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaagga cctcgccgtc	1080
ttggcctcga gggaggggct agacctcgtg cccggggacg accccatgct cctcgccctac	1140

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gtggcggtct	tggccaagga	ggccatggag	aaggcctatc	ccctcgccgt	gccccctggag	2460
gtggagggtg	ggatggggga	ggactggctt	tccgccaagg	gtcaccacca	ccaccaccac	2520

<210> 542

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 542

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
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 Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
 20 25 30  
 Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
 35 40 45  
 Phe Ala Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Ala Val  
 50 55 60  
 Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr  
 65 70 75 80  
 Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg  
 85 90 95  
 Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg  
 100 105 110  
 Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala  
 115 120 125  
 Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp  
 130 135 140  
 Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro  
 145 150 155 160  
 Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu  
 165 170 175  
 Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser  
 180 185 190  
 Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys  
 195 200 205  
 Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp  
 210 215 220  
 Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp  
 225 230 235 240  
 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu  
 245 250 255

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys  
                   260                                  265                                  270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
                   275                                  280                                  285

Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro  
                   290                                  295                                  300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp  
 305                                  310                                  315                                  320

Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg  
                                   325                                  330                                  335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly  
                                   340                                  345                                  350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp  
                   355                                  360                                  365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
                   370                                  375                                  380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385                                  390                                  395                                  400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
                                   405                                  410                                  415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
                                   420                                  425                                  430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
                   435                                  440                                  445

Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
                   450                                  455                                  460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala  
 465                                  470                                  475                                  480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
                                   485                                  490                                  495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly

500					505					510					
Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His
		515					520					525			
Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys
	530					535					540				
Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly
545					550					555					560
Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu
				565					570					575	
Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu
			580					585					590		
Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu
		595					600					605			
Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu
	610					615					620				
Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile
625					630					635					640
His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val
				645					650					655	
Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu
			660					665					670		
Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr
		675					680					685			
Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys
	690					695					700				
Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly
705					710					715					720
Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn
				725					730					735	
Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn
			740					745					750		



Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val  
755 760 765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln  
770 775 780

Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu  
785 790 795 800

Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala  
805 810 815

Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala  
820 825 830

Lys Gly His His His His His His  
835 840

<210> 543

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 543

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ggccaccacc tggcctaccg caccttcttt gccctgaagg gcctcaccac cagccggggg	120
gagccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct cagagaggac	180
ggggacgcgg tgatcgtggt ctttgacgcc gagggcccct ccttccgcca cgaggcctac	240
gggggggtaca aggcggggccg ggccccccacg ccggaggact ttccccggca actcgccctc	300
atcaaggagc tgggtggacct cctgggggttc acgcgcctcg aggtcccggg ctacgaggcg	360
gacgacgtcc tggccaccct ggccaagaag gcggaaaagg agggctacga ggtccgcatc	420
ctcaccgccg acaaagacct ttaccagctc ctttccgacc gcatccacgt cctccacccc	480
gaggggtacc tcatcacccc ggcttggtt tgggaaaagt acggcctgag gcccgaccag	540
tggggccgact accggggcct gaccggggac gagtccgaca accttcccgg ggtcaagggc	600
atcggggaga agacggcgct caagcttctg aaggagtggg ggagcctgga agccctcctc	660
aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggccca catggacgat	720

ctgaagctct cctgggacct ggccaaggtg cgcaccgacc tgcccttga ggtggacttc	780
gccaaaaggc gggagcccga ccgggagggg cttaaggcct ttctggagag gcttgagttt	840
ggcagcctcc tccacgagtt cggccttctg ggaggggaga agccccggga ggaggcccc	900
tggccccgc cggaaggggc cttcgtgggc tttgtgcttt ccgcaagga gcccatgtgg	960
gccgatcttc tggccctggc cgcctgcagg ggcggccgcg tgcaccgggc agcagacccc	1020
ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaagga cctcgccgtc	1080
ttggcctcga gggaggggct agacctcgtg cccggggacg accccatgct cctcgccctac	1140
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acggaggacg ccgcccaccg ggccctcctc tcggagaggc tccatcgga cctccttaag	1260
cgcctcgagg gggaggagaa gctcctttgg ctctaccacg aggtggaaaa gccctctcc	1320
cgggtccttg cccatatgga ggccaccggg gtacggcggg acgtggccta ccttcaggcc	1380
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aggcttccc ccttgaagaa gacgaagaag acaggcaagc gctccaccag cgccgcggtg	1560
ctggaggccc tacgggaggc ccaccccatc gtggagaaga tcctccagca ccgggagctc	1620
accaagctca agaacaccta cgtggacccc ctcccaagcc tcgtccaccc gaggacgggc	1680
cgcctccaca ccgcttcaa ccagacggcc acggccacgg ggaggcttag tagctccgac	1740
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cacaccaga ccgcaagctg gatgttcggc gtcccccccg aggccgtgga cccctgatg	1980
cgcggggcgg ccaagacggt gaacttcggc gtcctctacg gcatgtccgc ccataggctc	2040
tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa	2100
agcttcccca aggtgcgggc ctggatagaa aagacctg aggaggggag gaagcggggc	2160
tacgtgga aa ccctcttcgg aagaaggcgc tacgtgcccc acctcaacgc ccgggtgaag	2220
agcgtcaggg aggccgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc	2280
gacctcatga agctcgccat ggtgaagctc tttccccgcc tccgggagat gggggccgc	2340
atgctcctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag	2400
gtggcggtt tggccaagga ggccatggag aaggcctatc ccctcgccgt gccctggag	2460
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<210> 544

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 544

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Ala Val  
50 55 60

Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr  
65 70 75 80

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg  
85 90 95

Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg  
100 105 110

Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala  
115 120 125

Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp  
130 135 140

Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro  
145 150 155 160

Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu  
165 170 175

Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser  
180 185 190

Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys  
 195 200 205

Leu Leu Lys Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp  
 210 215 220

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp  
 225 230 235 240

Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu  
 245 250 255

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys  
 260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
 275 280 285

Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro  
 290 295 300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp  
 305 310 315 320

Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg  
 325 330 335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly  
 340 345 350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp  
 355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
 405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
 435 440 445

Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
 450 455 460  
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala  
 465 470 475 480  
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495  
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly  
 500 505 510  
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His  
 515 520 525  
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys  
 530 535 540  
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly  
 545 550 555 560  
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
 565 570 575  
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
 580 585 590  
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu  
 595 600 605  
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
 610 615 620  
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile  
 625 630 635 640  
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val  
 645 650 655  
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670  
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
 675 680 685  
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys

690	695	700
Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly 705 710 715 720		
Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn 725 730 735		
Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn 740 745 750		
Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val 755 760 765		
Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln 770 775 780		
Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu 785 790 795 800		
Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala 805 810 815		
Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala 820 825 830		
Lys Gly His His His His His His 835 840		

<210> 545

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 545

ggggagaaga cggcgctcag gcttctgaag gagtggggga gcctggaagc

50

<210> 546

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 546

gcttccaggc tcccccactc cttcagaagc ttgagcgccg ttttctcccc

50

<210> 547

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 547

ctggtcggga cggacgccaa tgaggggtgtg aag

33

<210> 548

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 548

gtccgtcccg accagaat

18

<210> 549

<211> 1008

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

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<400> 549
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ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg      120
cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga      180
atcctataca gagtctccaa catggctcga gtgggaatca ggccggtggt tgtattcgac      240
ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtctgag      300
gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct      360
caggctgcag ggagggttga cgagtacatt gttgactccg caaagacgct ttttaagttac      420
atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca      480
gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc      540
ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc      600
tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctggggttg      660
acgagggagc agctcatcga catagcgatt ctggtcggga cggacgccaa tgagggtgtg      720
aagggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tattttcagg      780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg      840
aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc      900
atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttggag      960
aagctcaaag ctctgaagtc aaccaggcc acgcttgaga ggtgggttc      1008

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<210> 550

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 550

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Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
1           5           10          15

```

```

Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
          20          25          30

```

```

Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
35          40          45

```



Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg  
 50 55 60  
 Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp  
 65 70 75 80  
 Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys  
 85 90 95  
 Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly  
 100 105 110  
 Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu  
 115 120 125  
 Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro  
 130 135 140  
 Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala  
 145 150 155 160  
 Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu  
 165 170 175  
 Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys  
 180 185 190  
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile  
 195 200 205  
 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln  
 210 215 220  
 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Ala Asn Glu Gly Val  
 225 230 235 240  
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly  
 245 250 255  
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val  
 260 265 270  
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr  
 275 280 285  
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu

290	295	300	
Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu			
305	310	315	320
Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe			
	325	330	335

<210> 551

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 551

ctggtcggga cggacaggaa tgagggtgtg aag 33

<210> 552

<211> 1008

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 552

atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca 60

ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg 120

cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga 180

atcctataca gagtctccaa catggctcgag gtgggaatca ggccggtggt tgtattcgac 240

ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtgag 300

gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct 360

caggctgcag ggagggttga cgagtacatt gttgactccg caaagacgct tttaagttac 420

atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca 480

gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc 540

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ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc      600
tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctggggttg      660
acgaggggagc agctcatcga catagcgatt ctggtcggga cggacaggaa tgaggggtgtg      720
aaggggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tatttttcagg      780
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg      840
aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc      900
atcgagttcc tgtgcgagga gcacgacttc agcaggggaga gggtcgagaa ggccttggag      960
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<210> 553

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 553

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Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
1           5           10           15

```

```

Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
          20           25           30

```

```

Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
          35           40           45

```

```

Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
          50           55           60

```

```

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
65           70           75           80

```

```

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
          85           90           95

```

```

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
          100          105          110

```

```

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu

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115	120	125
Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro 130 135 140		
Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala 145 150 155 160		
Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu 165 170 175		
Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys 180 185 190		
Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile 195 200 205		
Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln 210 215 220		
Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Arg Asn Glu Gly Val 225 230 235 240		
Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly 245 250 255		
Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val 260 265 270		
Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr 275 280 285		
Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu 290 295 300		
Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu 305 310 315 320		
Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe 325 330 335		

<210> 554

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 554  
gaaccacctc tcaagcgtgg 20

<210> 555

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 555  
acgcttgaga ggtgggttcct ggaggaggcc ccctgg 36

<210> 556

<211> 1011

<212> DNA

<213> Archaeoglobus fulgidus

<400> 556  
atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca 60  
ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg 120  
cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga 180  
atcctataca gagtctccaa catggtcgag gtgggaatca ggccggtgtt tgtattcgac 240  
ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtgag 300  
gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct 360  
caggctgcag ggagggttga cgagtacatt gttgactccg caaagacgct tttaagttac 420  
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<400> 557

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<211> 2643

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

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<210> 560

<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 560

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Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys  
35 40 45

Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg  
50 55 60

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp  
65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys  
85 90 95

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly  
100 105 110

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu  
115 120 125

Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro  
130 135 140

Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala  
145 150 155 160

Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu  
165 170 175

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys  
180 185 190

Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile  
195 200 205

Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln  
210 215 220

Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val  
225 230 235 240

Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly  
 245 250 255  
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val  
 260 265 270  
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr  
 275 280 285  
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu  
 290 295 300  
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu  
 305 310 315 320  
 Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe  
 325 330 335  
 Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe  
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 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala  
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 Ala Cys Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly  
 370 375 380  
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 385 390 395 400  
 Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro  
 405 410 415  
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly  
 420 425 430  
 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg  
 435 440 445  
 Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu  
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 Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu  
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 Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val

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Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile				
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Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile				
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Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys  
740 745 750

Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly  
755 760 765

Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg  
770 775 780

Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala  
785 790 795 800

Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg  
805 810 815

Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu  
820 825 830

Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu  
835 840 845

Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val  
850 855 860

Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His  
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His

<210> 561

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 561

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<210> 562

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

<400> 562

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<210> 563

<211> 2619

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 563

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<210> 564

<211> 873

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 564

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Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys  
35 40 45

Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg  
50 55 60

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp  
65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys  
85 90 95

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly  
100 105 110

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu  
115 120 125

Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro  
130 135 140

Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala  
145 150 155 160

Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu  
165 170 175

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys  
180 185 190

Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile  
195 200 205

Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln  
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Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val  
 225 230 235 240

Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly  
 245 250 255

Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val  
 260 265 270

Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr  
 275 280 285

Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu  
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Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu  
 305 310 315 320

Lys Leu Lys Ala Leu Lys Ser Thr Leu Glu Glu Ala Pro Trp Pro Pro  
 325 330 335

Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met  
 340 345 350

Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His  
 355 360 365

Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg  
 370 375 380

Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu  
 385 390 395 400

Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp  
 405 410 415

Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu  
 420 425 430

Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His  
 435 440 445

Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu  
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Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu

465		470		475		480
Ala Thr Gly Val Arg	Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu	485		490		495
Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu		500		505		510
Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val		515		520		525
Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr		530		535		540
Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala		545		550		555
His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu		565		570		575
Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr		580		585		590
Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg		595		600		605
Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro		610		615		620
Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala		625		630		635
Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His		645		650		655
Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp		660		665		670
Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala		675		680		685
Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val		690		695		700
Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro		705		710		715
						720

Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro  
725 730 735

Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg  
740 745 750

Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu  
755 760 765

Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe  
770 775 780

Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met  
785 790 795 800

Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu  
805 810 815

Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu  
820 825 830

Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu  
835 840 845

Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser  
850 855 860

Ala Lys Gly His His His His His His  
865 870

<210> 565

<211> 2643

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 565

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cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga	180
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ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtgag	300
gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct	360
caggctgcag ggaggggtga cgagtacatt gttgactccg caaagacgct ttttaagttac	420
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gtgctggccc acctctccgg cgacgagaac ctgatccggg tcttccagga ggggcgggac	2040
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<210> 566

<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 566

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Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys  
 35 40 45

Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg  
 50 55 60

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp  
 65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys  
 85 90 95

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly

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Asp	Lys	Asp	Ala	Lys	Lys	Tyr	Ala	Gln	Ala	Ala	Gly	Arg	Val	Asp	Glu
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Tyr	Ile	Val	Asp	Ser	Ala	Lys	Thr	Leu	Leu	Ser	Tyr	Met	Gly	Ile	Pro
	130					135					140				
Phe	Val	Asp	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	Ala
145					150					155					160
Ala	Lys	Gly	Asp	Val	Glu	Tyr	Thr	Gly	Ser	Gln	Asp	Tyr	Asp	Ser	Leu
				165					170					175	
Leu	Phe	Gly	Ser	Pro	Arg	Leu	Ala	Arg	Asn	Leu	Ala	Ile	Thr	Gly	Lys
			180					185					190		
Arg	Lys	Leu	Pro	Gly	Lys	Asn	Val	Tyr	Val	Asp	Val	Lys	Pro	Glu	Ile
		195					200					205			
Ile	Ile	Leu	Glu	Ser	Asn	Leu	Lys	Arg	Leu	Gly	Leu	Thr	Arg	Glu	Gln
	210					215					220				
Leu	Ile	Asp	Ile	Ala	Ile	Leu	Val	Gly	Thr	Asp	Tyr	Asn	Glu	Gly	Val
225					230					235					240
Lys	Gly	Val	Gly	Val	Lys	Lys	Ala	Leu	Asn	Tyr	Ile	Lys	Thr	Tyr	Gly
				245					250					255	
Asp	Ile	Phe	Arg	Ala	Leu	Lys	Ala	Leu	Lys	Val	Asn	Ile	Asp	His	Val
			260					265					270		
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		275					280					285			
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	290					295					300				
Cys	Glu	Glu	His	Asp	Phe	Ser	Arg	Glu	Arg	Val	Glu	Lys	Ala	Leu	Glu
305					310					315					320
Lys	Leu	Lys	Ala	Leu	Lys	Ser	Thr	Gln	Ala	Thr	Leu	Glu	Arg	Trp	Phe
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Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe
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Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala  
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Ala Cys Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala  
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385 390 395 400  
Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro  
405 410 415  
Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly  
420 425 430  
Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg  
435 440 445  
Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Leu Lys Arg Leu Glu  
450 455 460  
Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu  
465 470 475 480  
Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val  
485 490 495  
Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg  
500 505 510  
Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn  
515 520 525  
Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro  
530 535 540  
Ala Ile Lys Lys Thr Gln Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala  
545 550 555 560  
Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu  
565 570 575  
Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu  
580 585 590  
Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn  
595 600 605

Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu  
 610 615 620

Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala  
 625 630 635 640

Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln  
 645 650 655

Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile  
 660 665 670

Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp  
 675 680 685

Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala  
 690 695 700

Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg  
 705 710 715 720

Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile  
 725 730 735

Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys  
 740 745 750

Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly  
 755 760 765

Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg  
 770 775 780

Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala  
 785 790 795 800

Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu  
 805 810 815

Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Val Leu  
 820 825 830

Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu  
 835 840 845

Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val



850

855

860

Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu His His His His His  
 865 870 875 880

His

&lt;210&gt; 567

&lt;211&gt; 2643

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic

&lt;400&gt; 567

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cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga      180
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<210> 568

<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 568

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35 40 45

Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg  
50 55 60

Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp  
65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys  
85 90 95

Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly  
100 105 110

Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu  
115 120 125

Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro  
130 135 140

Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala  
145 150 155 160

Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu  
165 170 175

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys  
180 185 190

Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile  
195 200 205

Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln  
210 215 220

Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val  
 225 230 235 240  
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly  
 245 250 255  
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val  
 260 265 270  
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr  
 275 280 285  
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu  
 290 295 300  
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu  
 305 310 315 320  
 Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe  
 325 330 335  
 Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe  
 340 345 350  
 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala  
 355 360 365  
 Ala Cys Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala  
 370 375 380  
 Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser  
 385 390 395 400  
 Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro  
 405 410 415  
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly  
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 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg  
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 Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu  
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 Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu

465		470		475		480									
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Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn
		515					520					525			
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Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	Thr	Tyr	Ile	Asp	Pro	Leu
			580					585					590		
Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn
		595					600					605			
Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu
	610					615						620			
Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala
625					630					635					640
Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln
			645						650					655	
Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile
			660					665					670		
Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Glu	Thr	Ala	Ser	Trp
		675					680					685			
Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala
	690					695					700				
Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg
705					710					715					720

Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile  
725 730 735

Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys  
740 745 750

Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly  
755 760 765

Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg  
770 775 780

Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala  
785 790 795 800

Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu  
805 810 815

Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asn Glu Leu Val Leu  
820 825 830

Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu  
835 840 845

Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val  
850 855 860

Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu His His His His His  
865 870 875 880

His

<210> 569

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 569

gagcggataa caatttcaca cagg

24

<210> 570

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 570

tgcccgggtgc acgcggccgc ccctgcaggc

30

<210> 571

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 571

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ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc	120
caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg	180
gtgatcgtgg tgtttgacgc caaggccccc tccttccgcc accagacctt cgaggcctac	240
aaggcggggg gggctccac ccccgaggac tttcccggc agcttgccct tatcaaggag	300
atggtggacc ttttgggcct ggagcgcctc gaggtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaaaag gagggctacg aggtccgcat cctcaccgcc	420
gacaaagacc tttaccagct cctttccgac cgcattccacg tcctccaccc cgaggggtac	480
ctcatcaccc cggcctggct ttgggaaaag tacggcctga ggcccgacca gtgggcccac	540
taccggggcc tgaccgggga cgagtccgac aaccttcccg ggggtcaagg catcgaggag	600
aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg	660
gaccggctga agcccgccat ccgggagaag atcctggccc acatggacga tctgaagctc	720
tcctgggacc tggccaaggt gcgcaccgac ctgcccctgg aggtggactt cgccaaaagg	780
cgggagcccg accgggaggg ggagaagccc cgggaggagg cccctggcc cccgcccga	840
ggggccttcg tgggcttcct cctttccgc cccgagccca tgtgggcgga gcttaaagcc	900

ctggccgcct gcaggggcgg ccgcgtgcac cgggcagcag accccttggc ggggctaaag	960
gacctcaagg aggtccgggg cctcctcgcc aaggacctcg ccgtcttggc ctcgagggag	1020
gggctagacc tcgtgcccgg ggacgacccc atgtcctcgc cctacctcct ggacccttcg	1080
aacaccaccc ccgaggggggt ggcgcggcgc tacggggggg agtggacgga ggacgccgcc	1140
caccggggccc tcctctcgga gaggtccat cggaacctcc ttaagcgct cgagggggag	1200
gagaagctcc tttggctcta ccacgaggtg gaaaagcccc tctcccggt cctggcccat	1260
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gcggaggaga tccgccgcct cgaggaggag gtcttcgcgt tggcgggcca ccccttcaac	1380
ctcaactccc gggaccagct ggaaaggggt ctctttgacg agcttaggct tccgccttg	1440
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gaggcccacc ccatcgtgga gaagatctc cagcaccggg agctcacaa gctcaagaac	1560
acctacgtgg accccctccc aagcctcgtc caccgagga cgggccgcct ccacaccgc	1620
ttcaaccaga cggccacggc cacggggagg cttagtagct ccgaccccaa cctgcagaac	1680
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tgggcgttgg tggccctgga ctatagccag atagagctcc gcgtcctcgc ccacctctcc	1800
ggggacgaaa acctgatcag ggtcttcag gaggggaagg acatccacac ccagaccgca	1860
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acggtgaact tcggcgtcct ctacggcatg tccgccata ggctctcca ggagcttgcc	1980
atcccctacg aggaggcggg ggcctttata gagcgctact tccaaagctt cccaagggtg	2040
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ttcgaagaa ggcgctacgt gcccgaacct aacgcccggg tgaagagcgt caggagggcc	2160
gcggagcgca tggccttcaa catgcccgtc cagggcaccg ccgccgacct catgaagctc	2220
gccatggtga agctcttccc ccgcctccgg gagatggggg ccgcgatgct cctccaggtc	2280
gccaacgagc tcctcctgga ggcccccaa gcgcggggcg aggaggtggc ggctttggcc	2340
aaggaggcca tggagaaggc ctatcccctc gccgtgcccc tggaggtgga ggtggggatg	2400
ggggaggact ggctttccgc caagggtcac caccaccacc accac	2445

<210> 572

<211> 815

<212> PRT

<213> Artificial Sequence



<220>

<223> Synthetic

<400> 572

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val  
1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu  
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys  
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val  
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr  
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
85 90 95

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val  
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala  
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu  
130 135 140

Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr  
145 150 155 160

Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp  
165 170 175

Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu  
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu  
195 200 205

Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys  
210 215 220

Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu  
 225 230 235 240

Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp  
 245 250 255

Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu  
 260 265 270

Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu  
 275 280 285

Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys  
 290 295 300

Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys  
 305 310 315 320

Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu  
 325 330 335

Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu  
 340 345 350

Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala  
 355 360 365

Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu  
 370 375 380

Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu  
 385 390 395 400

Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg  
 405 410 415

Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr  
 420 425 430

Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu  
 435 440 445

Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg  
 450 455 460

Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu  
 465 470 475 480

Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu  
 485 490 495  
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His  
 500 505 510  
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser  
 515 520 525  
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr  
 530 535 540  
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn  
 545 550 555 560  
 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val  
 565 570 575  
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu  
 580 585 590  
 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val  
 595 600 605  
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe  
 610 615 620  
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys  
 625 630 635 640  
 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser  
 645 650 655  
 Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg  
 660 665 670  
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu  
 675 680 685  
 Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg  
 690 695 700  
 Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala  
 705 710 715 720  
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp

	725		730		735
Leu Met Lys	Leu Ala Met Val Lys	Leu Phe Pro Arg	Leu Arg Glu Met		
	740	745	750		
Gly Ala Arg	Met Leu Leu Gln Val	Ala Asn Glu Leu	Leu Leu Glu Ala		
	755	760	765		
Pro Gln Ala	Arg Ala Glu Glu Val	Ala Ala Leu Ala	Lys Glu Ala Met		
	770	775	780		
Glu Lys Ala	Tyr Pro Leu Ala Val	Pro Leu Glu Val	Glu Val Gly Met		
	785	790	795	800	
Gly Glu Asp	Trp Leu Ser Ala Lys	Gly His His His	His His His		
	805	810	815		

<210> 573

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 573

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ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct caaggaggac	180
ggggacgcgg tgatcgtggt ctttgacgcc aaggccccct ccttcgcga cgaggcctac	240
ggggggtaca aggcggggccg ggccccacc ccggaggact tccccgcca gtcgccttg	300
gtcaagcggc tggtagacct tctgggcctg gtccgcctcg aggccccggg gtacgaggcg	360
gacgacgtcc tgggcaccct ggccaagaag gccgaaaagg aggggtacga ggtgcgcac	420
ctcaccgccc accgcgacct ctaccaactc gtctccgacc gcatccacgt cctccacccc	480
gaggggtacc tcatcacccc ggagtggctt tgggagaagt atgggcttaa gccttcccag	540
tgggtggact accgggcctt ggccggggac ccttcgcaca acatccccgg cgtgaagggc	600
atcggggaga agacggcggc caagctgac cgaggagtggg gaagcctgga aaacctctc	660
aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggccca catggacgat	720

ctgaagctct cctgggacct ggccaaggtg cgcaccgacc tgccccctgga ggtggacttc	780
gccaaaaggc gggagcccgga ccgggagagg cttagggcct ttctggagag gcttgagttt	840
ggcagcctcc tccacgagtt cggccttctg gaaagcccca aggccctgga ggaggccccc	900
tggccccgc cggaaggggc cttcgtgggc ttcgtcctct cccgccccga gcccatgtgg	960
gcgagactta aagccctggc cgctgcagg ggcggccgcg tgcaccgggc agcagacccc	1020
ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaagga cctcgccgtc	1080
ttggcctcga gggaggggct agacctcgtg cccggggacg accccatgct cctcgccctac	1140
ctcctggacc cttcgaacac ccccccgag ggggtggcgc ggcgctacgg gggggagtg	1200
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aggcttcccg ccttgaagaa gacgaagaag acaggcaagc gctccaccag cgccgcggtg	1560
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accaagctca agaacaccta cgtggacccc ctccaagcc tcgtccacc gaggacgggc	1680
cgcctccaca cccgcttcaa ccagacggcc acggccacgg ggaggcttag tagctccgac	1740
cccaacctgc agaacatccc cgtccgcacc cccttgggccc agaggatccg ccgggccttc	1800
gtggccgagg cgggttgggc gttggtggcc ctggactata gccagataga gctccgcgtc	1860
ctcgcccacc tctccgggga cgaaaacctg atcagggtct tccaggagg gaaggacatc	1920
cacaccaga ccgcaagctg gatgttcggc gtccccccgg aggccgtgga cccctgatg	1980
cgccgggcgg ccaagacggt gaacttcggc gtccctctac gcatgtccgc ccataggctc	2040
tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa	2100
agcttcccca aggtgcgggc ctggatagaa aagaccctgg aggaggggag gaagcggggc	2160
tacgtggaaa ccctcttcgg aagaaggcgc tacgtgccc acctcaacgc ccgggtgaag	2220
agcgtcaggg aggccgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc	2280
gacctcatga agctcgccat ggtgaagctc ttcccccgcc tccgggagat gggggcccg	2340
atgctcctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag	2400
gtggcggtct tggccaagga ggccatggag aaggcctatc ccctcgccgt gccctggag	2460
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<210> 574

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 574

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val  
50 55 60

Ile Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr  
65 70 75 80

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg  
85 90 95

Gln Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg  
100 105 110

Leu Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala  
115 120 125

Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp  
130 135 140

Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Ile His Val Leu His Pro  
145 150 155 160

Glu Gly Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu  
165 170 175

Lys Pro Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser  
180 185 190

Asp Asn Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys  
 195 200 205

Leu Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp  
 210 215 220

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp  
 225 230 235 240

Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu  
 245 250 255

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg  
 260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
 275 280 285

Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro  
 290 295 300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp  
 305 310 315 320

Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg  
 325 330 335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly  
 340 345 350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp  
 355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
 405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
 435 440 445

Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
 450 455 460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala  
 465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly  
 500 505 510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His  
 515 520 525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys  
 530 535 540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly  
 545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
 565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
 580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu  
 595 600 605

Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
 610 615 620

Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile  
 625 630 635 640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val  
 645 650 655

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
 675 680 685

Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys



690		695		700
Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly				
705		710		715 720
Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn				
		725	730	735
Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn				
		740	745	750
Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val				
		755	760	765
Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln				
		770	775	780
Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu				
785		790	795	800
Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala				
		805	810	815
Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala				
		820	825	830
Lys Gly His His His His His His				
		835	840	
<210>	575			
<211>	2445			
<212>	DNA			
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<220>				
<223>	Synthetic			
<400>	575			
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caggcggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg				180
gtgatcgtgg tgtttgacgc caaggccccc tccttccgcc accagacctt cgaggcctac				240

aaggcggggc	gggctccac	ccccgaggac	tttccccggc	agcttgccct	tatcaaggag	300
atggtggacc	ttttgggctt	taccgcctc	gaggtgccg	gctttgaagc	ggatgacgtc	360
ctggctaccc	tggccaagaa	ggcggaaaag	gagggctacg	aggtccgcat	cctcaccgcc	420
gacaaagacc	tttaccagct	cctttccgac	cgcatccacg	tctccacccc	cgaggggtac	480
ctcatcaccc	cggcctggct	ttgggaaaag	tacggcctga	ggcccagcca	gtggggccgac	540
taccgggccc	tgaccgggga	cgagtccgac	aaccttcccc	gggtcaagg	catcggggag	600
aagacggcga	ggaagcttct	ggaggagtgg	gggagcctgg	aagccctcct	caagaacctg	660
gaccggtga	agcccgccat	ccgggagaag	atcctggccc	acatggacga	tctgaagctc	720
tcttgggacc	tggccaaggt	gcgcaccgac	ctgcccctgg	aggtggactt	cgccaaaagg	780
cgggagccc	accgggaggg	ggagaagccc	cgggaggagg	ccccctggcc	cccggccgaa	840
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gacctcaagg	aggtccgggg	cctcctcgcc	aaggacctcg	ccgtcttggc	ctcgaggggag	1020
gggctagacc	tcgtgcccg	ggacgacccc	atgctcctcg	cctacctcct	ggaccttctg	1080
aacaccaccc	ccgaggggg	ggcgcggcgc	tacggggggg	agtggacgga	ggacgccgcc	1140
caccgggccc	tctctcga	gaggctccat	cggaacctcc	ttaagcgct	cgagggggag	1200
gagaagctcc	tttggtcta	ccacgagggtg	gaaaagcccc	tctccgggt	cctggcccat	1260
atggaggcca	ccggggtacg	gcgggacgtg	gcctaccttc	aggccctttc	cctggagctt	1320
gcggaggaga	tccgccgcct	cgaggaggag	gtcttccgct	tggcgggcca	ccccttcaac	1380
ctcaactccc	gggaccagct	ggaaagggtg	ctctttgacg	agcttaggct	tccgccttg	1440
aagaagacga	agaagacagg	caagcgctcc	accagcgccg	cgggtgctgga	ggccctacgg	1500
gaggcccacc	ccatcggtga	gaagatcctc	cagcaccggg	agctcaccaa	gctcaagaac	1560
acctacgtgg	acccctccc	aagcctcgtc	caccgagga	cgggcgcct	ccacaccgc	1620
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ggggacgaaa	acctgatcag	ggtcttccag	gaggggaagg	acatccacac	ccagaccgca	1860
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acggtgaact	tcggcgctct	ctacggcatg	tccgcccata	ggctctccca	ggagcttgcc	1980
atcccctacg	aggaggcggt	ggcctttata	gagcgctact	tccaaagctt	ccccaagggtg	2040
cgggcctgga	tagaaaagac	cctggaggag	gggaggaagc	ggggctacgt	ggaaaccctc	2100

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ttcggaagaa ggcgctacgt gcccgcacctc aacgcccggg tgaagagcgt cagggaggcc 2160
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<210> 576

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 576

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Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
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Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
          20           25           30

```

```

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
      35           40           45

```

```

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50           55           60

```

```

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65           70           75           80

```

```

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
          85           90           95

```

```

Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val
100           105           110

```

```

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115           120           125

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```

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu

```

130		135		140											
Tyr 145	Gln	Leu	Leu	Ser	Asp 150	Arg	Ile	His	Val	Leu 155	His	Pro	Glu	Gly	Tyr 160
Leu	Ile	Thr	Pro	Ala 165	Trp	Leu	Trp	Glu	Lys 170	Tyr	Gly	Leu	Arg	Pro	Asp 175
Gln	Trp	Ala	Asp 180	Tyr	Arg	Ala	Leu	Thr 185	Gly	Asp	Glu	Ser	Asp 190	Asn	Leu
Pro	Gly	Val 195	Lys	Gly	Ile	Gly	Glu 200	Lys	Thr	Ala	Arg	Lys 205	Leu	Leu	Glu
Glu	Trp 210	Gly	Ser	Leu	Glu	Ala 215	Leu	Leu	Lys	Asn	Leu 220	Asp	Arg	Leu	Lys
Pro	Ala	Ile	Arg	Glu	Lys 230	Ile	Leu	Ala	His	Met 235	Asp	Asp	Leu	Lys	Leu 240
Ser	Trp	Asp	Leu	Ala 245	Lys	Val	Arg	Thr	Asp 250	Leu	Pro	Leu	Glu	Val 255	Asp
Phe	Ala	Lys	Arg 260	Arg	Glu	Pro	Asp	Arg 265	Glu	Gly	Glu	Lys	Pro	Arg	Glu 270
Glu	Ala 275	Pro	Trp	Pro	Pro	Pro	Glu 280	Gly	Ala	Phe	Val	Gly 285	Phe	Leu	Leu
Ser	Arg 290	Pro	Glu	Pro	Met	Trp 295	Ala	Glu	Leu	Lys	Ala 300	Leu	Ala	Ala	Cys
Arg 305	Gly	Gly	Arg	Val	His 310	Arg	Ala	Ala	Asp	Pro 315	Leu	Ala	Gly	Leu	Lys 320
Asp	Leu	Lys	Glu	Val 325	Arg	Gly	Leu	Leu	Ala 330	Lys	Asp	Leu	Ala	Val 335	Leu
Ala	Ser	Arg	Glu 340	Gly	Leu	Asp	Leu	Val 345	Pro	Gly	Asp	Asp	Pro	Met	Leu 350
Leu	Ala	Tyr 355	Leu	Leu	Asp	Pro	Ser 360	Asn	Thr	Thr	Pro	Glu 365	Gly	Val	Ala
Arg 370	Arg	Tyr	Gly	Gly	Glu	Trp 375	Thr	Glu	Asp	Ala	Ala 380	His	Arg	Ala	Leu

Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu  
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 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr  
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 Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg  
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 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu  
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 Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu  
 485 490 495  
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His  
 500 505 510  
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser  
 515 520 525  
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr  
 530 535 540  
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn  
 545 550 555 560  
 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val  
 565 570 575  
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu  
 580 585 590  
 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val  
 595 600 605  
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe  
 610 615 620  
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys  
 625 630 635 640

Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser  
645 650 655

Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg  
660 665 670

Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu  
675 680 685

Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg  
690 695 700

Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala  
705 710 715 720

Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp  
725 730 735

Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met  
740 745 750

Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala  
755 760 765

Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met  
770 775 780

Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met  
785 790 795 800

Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His  
805 810 815

<210> 577

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 577

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ggggggtaca	aggcggggccg	ggccccacc	ccggaggact	tccccgcgca	gctcgccttg	300
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ctcaccgccg	accgcgacct	ctaccaactc	gtctccgacc	gcatccacgt	cctccacccc	480
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<210> 578

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 578

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 20 25 30

Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
 35 40 45

Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val  
 50 55 60

Ile Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr  
 65 70 75 80

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg  
 85 90 95

Gln Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Phe Thr Arg



100					105					110					
Leu	Glu	Ala	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Gly	Thr	Leu	Ala
		115					120					125			
Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp
	130					135					140				
Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro
145				150						155					160
Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu
				165					170					175	
Lys	Pro	Ser	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser
			180					185					190		
Asp	Asn	Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys
		195					200					205			
Leu	Ile	Arg	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp
	210					215					220				
Arg	Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp
225					230					235					240
Leu	Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu
				245					250					255	
Glu	Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg
			260					265					270		
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly
		275					280					285			
Leu	Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro
	290					295					300				
Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp
305					310					315					320
Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Gly	Gly	Arg	Val	His	Arg
				325					330					335	
Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	Arg	Gly
			340				345						350		

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp  
 355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
 405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
 435 440 445

Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
 450 455 460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala  
 465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly  
 500 505 510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His  
 515 520 525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys  
 530 535 540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly  
 545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
 565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
 580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu  
 595 600 605

Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
610 615 620  
Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile  
625 630 635 640  
His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val  
645 650 655  
Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
660 665 670  
Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
675 680 685  
Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
690 695 700  
Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly  
705 710 715 720  
Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn  
725 730 735  
Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
740 745 750  
Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val  
755 760 765  
Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln  
770 775 780  
Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu  
785 790 795 800  
Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala  
805 810 815  
Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala  
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Lys Gly His His His His His His  
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<210> 579

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 579

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<210> 580

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 580

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Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		

Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			

Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50		55		60
Phe 65	Asp	Ala	Glu	Ala
	Pro	Ser	Phe	Arg
			His	Gln
				Thr
				Tyr
				Glu
				Ala
				Tyr 80
Lys	Ala	Gly	Arg	Ala
				Pro
				Thr
				Pro
				Glu
				Asp
				Phe
				Pro
				Arg
				Gln
				Leu
				Ala 95
Leu	Ile	Lys	Glu	Met
				Val
				Asp
				Leu
				Leu
				Gly
				Leu
				Glu
				Arg
				Leu
				Glu
				Val 110
Pro	Gly	Phe	Glu	Ala
				Asp
				Asp
				Val
				Leu
				Ala
				Thr
				Leu
				Ala
				Lys
				Lys
				Ala
Glu	Lys	Glu	Gly	Tyr
				Glu
				Val
				Arg
				Ile
				Leu
				Thr
				Ala
				Asp
				Lys
				Asp
				Leu
Tyr	Gln	Leu	Leu	Ser
				Asp
				Arg
				Ile
				His
				Val
				Leu
				His
				Pro
				Glu
				Gly
				Tyr 160
Leu	Ile	Thr	Pro	Ala
				Trp
				Leu
				Trp
				Glu
				Lys
				Tyr
				Gly
				Leu
				Arg
				Pro
				Asp 175
Gln	Trp	Ala	Asp	Tyr
				Arg
				Ala
				Leu
				Thr
				Gly
				Asp
				Glu
				Ser
				Asp
				Asn
				Leu 190
Pro	Gly	Val	Lys	Gly
				Ile
				Gly
				Glu
				Lys
				Thr
				Ala
				Arg
				Lys
				Leu
				Leu
				Glu 205
Glu	Trp	Gly	Ser	Leu
				Glu
				Ala
				Leu
				Leu
				Lys
				Asn
				Leu
				Asp
				Arg
				Leu
				Lys
Pro	Ala	Ile	Arg	Glu
				Lys
				Ile
				Leu
				Ala
				His
				Met
				Asp
				Asp
				Leu
				Lys
				Leu 240
Ser	Trp	Asp	Leu	Ala
				Lys
				Val
				Arg
				Thr
				Asp
				Leu
				Pro
				Leu
				Glu
				Val
				Asp 255
Phe	Ala	Lys	Arg	Arg
				Glu
				Pro
				Asp
				Arg
				Glu
				Gly
				Glu
				Lys
				Pro
				Arg
				Glu 270
Glu	Ala	Pro	Trp	Pro
				Pro
				Pro
				Glu
				Gly
				Ala
				Phe
				Val
				Gly
				Phe
				Leu
				Leu 285
Ser	Arg	Pro	Glu	Pro
				Met
				Trp
				Ala
				Glu
				Leu
				Lys
				Ala
				Leu
				Ala
				Ala
				Cys 300

Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys  
 305 310 315 320  
 Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu  
 325 330 335  
 Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu  
 340 345 350  
 Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala  
 355 360 365  
 Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu  
 370 375 380  
 Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu  
 385 390 395 400  
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg  
 405 410 415  
 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr  
 420 425 430  
 Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu  
 435 440 445  
 Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg  
 450 455 460  
 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu  
 465 470 475 480  
 Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu  
 485 490 495  
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His  
 500 505 510  
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser  
 515 520 525  
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr  
 530 535 540  
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn  
 545 550 555 560

Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val  
565 570 575

Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu  
580 585 590

Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val  
595 600 605

Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe  
610 615 620

Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys  
625 630 635 640

Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser  
645 650 655

Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg  
660 665 670

Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu  
675 680 685

Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg  
690 695 700

Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala  
705 710 715 720

Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp  
725 730 735

Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met  
740 745 750

Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala  
755 760 765

Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met  
770 775 780

Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met  
785 790 795 800

Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His



805

810

815

&lt;210&gt; 581

&lt;211&gt; 2445

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic

&lt;400&gt; 581

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ctggcctacc gtaccttttt tgccctgaag ggccctacca ccagccgcgg ggagccggtc	120
caggcggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg	180
gtgatcgtgg tctttgacgc cgaggccccc tccttcgcgc accagaccta cgaggcctac	240
aaggcggggc gggctccac ccccgaggac tttccccggc agcttgccct tatcaaggag	300
atggtggacc ttttgggctt taccgcctc gaggtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaaaag gagggctacg aggtccgcat cctcaccgcc	420
gacaaagacc tttaccagct cctttccgac cgcattccacg tcctccaccc cgaggggtac	480
ctcatcaccc cggcctggct ttgggaaaag tacggcctga ggcccgacca gtgggccgac	540
taccgggccc tgaccgggga cgagtccgac aaccttcccg gggtaaggga catcggggag	600
aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg	660
gaccggctga agcccgccat ccgggagaag atcctggccc acatggacga tctgaagctc	720
tcctgggacc tggccaaggt ggcacccgac ctgcccctgg aggtggactt cgccaaaagg	780
cgggagcccg accgggaggg ggagaagccc cgggaggagg ccccttgcc cccgcccga	840
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ctggccgcct gcaggggcgg ccgcgtgcac cgggcagcag accccttggc ggggctaaag	960
gacctcaagg aggtccgggg cctcctcgcc aaggacctcg ccgtcttggc ctcgaggag	1020
gggctagacc tcgtgcccgg ggacgacccc atgctcctcg cctacctcct ggaccttcg	1080
aacaccaccc ccgagggggg ggcgcggcgc tacggggggg agtggacgga ggacgccgcc	1140
caccgggccc tcctctcgga gaggtccat cggaaacctc ttaagcgctt cgagggggag	1200
gagaagctcc tttggctcta ccacgaggtg gaaaagcccc tctccgggt cctggcccat	1260
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 aagaagacga agaagacagg caagcgctcc accagcgccg cggtgctgga gggcctacgg 1500  
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 ttcggaagaa ggcgtacgt gcccacctc aacgccggg tgaagagcgt caggagggcc 2160  
 gcggagcgca tggccttcaa catgcccgtc cagggcaccg ccgccgacct catgaagctc 2220  
 gccatggtga agctcttccc ccgcctccgg gagatggggg ccgcgatgct cctccaggtc 2280  
 gccaacgagc tcctcctgga ggccccccaa gcgcggggcg aggaggtggc ggctttggcc 2340  
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 ggggaggact ggctttccgc caagggtcac caccaccacc accac 2445

<210> 582

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 582

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
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Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys  
 35 40 45  
 Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val  
 50 55 60  
 Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr  
 65 70 75 80  
 Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
 85 90 95  
 Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val  
 100 105 110  
 Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala  
 115 120 125  
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu  
 130 135 140  
 Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr  
 145 150 155 160  
 Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp  
 165 170 175  
 Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu  
 180 185 190  
 Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu  
 195 200 205  
 Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys  
 210 215 220  
 Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu  
 225 230 235 240  
 Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp  
 245 250 255  
 Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu  
 260 265 270  
 Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu  
 275 280 285

Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys  
 290 295 300

Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys  
 305 310 315 320

Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu  
 325 330 335

Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu  
 340 345 350

Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala  
 355 360 365

Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu  
 370 375 380

Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu  
 385 390 395 400

Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg  
 405 410 415

Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr  
 420 425 430

Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu  
 435 440 445

Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg  
 450 455 460

Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu  
 465 470 475 480

Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu  
 485 490 495

Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His  
 500 505 510

Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser  
 515 520 525

Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr

530		535		540
Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn				
545		550		555 560
Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val				
	565		570	575
Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu				
	580		585	590
Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val				
	595		600	605
Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe				
	610		615	620
Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys				
	625		630	635 640
Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser				
	645		650	655
Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg				
	660		665	670
Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu				
	675		680	685
Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg				
	690		695	700
Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala				
	705		710	715 720
Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp				
	725		730	735
Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met				
	740		745	750
Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala				
	755		760	765
Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met				
	770		775	780

Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met  
785 790 795 800

Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His  
805 810 815

<210> 583

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 583

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gagccggtcc aggcggtgta cgggtttgcc aagagccttt tgaaggcgct aagagaagac      180
ggggacgcgg tgatcgtggt ctttgacgcc gagggccctt ccttcgcga cgaggcctac      240
gggggggtaca aggcggggcg ggctccacc cccgaggact ttccccggca gcttgccctt      300
atcaaggagc tgggtggacct cctgggggtt accgcctcg aggtccccgg ctacgaggcg      360
gacgacgttc tcgccaccct ggccaagaag gcggaaaagg aggggtacga ggtgcgcatc      420
ctcaccgcgg acaaagacct ttaccagctc ctttcgcacc gcattccacgt cctccacccc      480
gaggggtacc tcatcacccc ggcttggtt tgggaaaagt acggcctgag gcccgaccag      540
tgggccgact accgggccct gaccggggac gaggccgaca accttcccgg ggtcaagggc      600
atcggggaga agaccgccct caagctcctc aaggagtggg ggagcctgga agccctcctc      660
aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggcca catggacgat      720
ctgaagctct cctgggacct ggccaaggtg cgcaccgacc tgcccctgga ggtggacttc      780
gccaaaaggc gggagcccga ccgggagggg cttaaggcct ttttggagag gctggagttc      840
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gccgatcttc tggccctggc cgcctgcagg ggcggccgcg tgcaaccggc agcagacccc     1020
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ttggcctcga gggaggggct agacctcgtg cccggggacg accccatgct cctcgccctac     1140
ctcctggacc cttcgaacac ccccccgag ggggtggcgc ggcgctacgg gggggagtgg     1200

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cgggtcctgg	cccatatgga	ggccaccggg	gtacggcggg	acgtggccta	ccttcaggcc	1380
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ctggaggccc	tacgggaggg	ccaccccatc	gtggagaaga	tcctccagca	ccgggagctc	1620
accaagctca	agaacaccta	cgtggacccc	ctcccaagcc	tcgtccaccc	gaggacgggc	1680
cgcctccaca	cccgttcaa	ccagacggcc	acggccacgg	ggaggcttag	tagctccgac	1740
cccaacctgc	agaacatccc	cgtccgcacc	cccttggggc	agaggatccg	ccgggccttc	1800
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agcttcccca	aggtgcgggc	ctggatagaa	aagaccttgg	aggaggggag	gaagcggggc	2160
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agcgtcaggg	aggccgcgga	gcgcatggcc	ttcaacatgc	ccgtccaggg	caccgcccgc	2280
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gtggcggtt	tggccaagga	ggccatggag	aaggcctatc	ccctcgccgt	gcccctggag	2460
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<210> 584

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 584

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val





Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys  
 260 265 270

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
 275 280 285

Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro  
 290 295 300

Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp  
 305 310 315 320

Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg  
 325 330 335

Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly  
 340 345 350

Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp  
 355 360 365

Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
 405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
 435 440 445

Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
 450 455 460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala  
 465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly  
 500 505 510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His  
515 520 525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys  
530 535 540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly  
545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu  
595 600 605

Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
610 615 620

Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile  
625 630 635 640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val  
645 650 655

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
675 680 685

Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
690 695 700

Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly  
705 710 715 720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn  
725 730 735

Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
740 745 750

Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val

755		760		765											
Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln
	770					775					780				
Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu
785					790					795				800	
Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala
				805					810					815	
Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala
			820					825					830		
Lys	Gly	His	His	His	His	His	His								
		835					840								

<210> 585

<211> 2499

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 585

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cagatggtct	acggcttcgc	ccggagcctc	ctcaaggcct	tgaaggagga	cggacaggcg	180
gtggtcgtgg	tctttgacgc	caaggccccc	tccttcgcgc	acgaggccta	cgaggcctac	240
aaggcggggc	gggccccccac	cccggaggac	ttccccggca	gctcgccctt	atcaaggaga	300
tggtggacct	tttgggcctg	gcgcgccctc	aggtcccggg	ctacgaggcg	gacgacgttc	360
tcgccaccct	ggccaagaag	gcggaaaagg	aggggtacga	ggtgcgcatt	ctaccgccga	420
ccgcgacctc	taccaactcg	tctccgaccg	cgtcgccgctc	ctccaccccg	agggccacct	480
catcaccctg	gagtggcttt	gggagaagta	cggcctcagg	ccggagcagt	gggtggactt	540
ccgcgccctc	gtggggggacc	cctccgacaa	cctccccggg	gtcaagggca	tcggggagga	600
gacggcggcc	aagctgatcc	gggagtgggg	aagcctggaa	aaccttctta	agcacctgga	660
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atccctggag ctatcccggg tgcacacgga cttgcttctt cagtggactt taaggccctg	780
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<210> 586

<211> 811

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 586

Met Glu Phe Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val  
1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu  
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys  
35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val  
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr  
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
85 90 95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val  
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala  
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Gly Asp Arg Asp Leu  
130 135 140

Tyr Gln Leu Val Ser Asp Arg Val Ala Arg Pro Glu Gln Trp Val Asp  
145 150 155 160

Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile Pro Gly Val Lys  
165 170 175

Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp Gly Ser  
180 185 190

Val Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala Ile Arg  
195 200 205

Glu Lys Ile Leu Ala His Met Glu Asp Leu Lys Leu Ser Leu Glu Leu  
210 215 220

Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val Asp Leu Ala Gln Gly  
225 230 235 240

Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe Leu Glu Arg Leu Glu  
245 250 255

Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro Val Ala  
260 265 270

Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Tyr  
275 280 285

Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Asn Ala Leu Ala  
290 295 300

Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly  
305 310 315 320

Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala  
325 330 335

Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro  
340 345 350

Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly  
355 360 365

Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg  
370 375 380

Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu  
385 390 395 400

Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu  
405 410 415

Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val  
420 425 430

Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg  
435 440 445

Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn  
 450 455 460

Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro  
 465 470 475 480

Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala  
 485 490 495

Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu  
 500 505 510

Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu  
 515 520 525

Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn  
 530 535 540

Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu  
 545 550 555 560

Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala  
 565 570 575

Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln  
 580 585 590

Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile  
 595 600 605

Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp  
 610 615 620

Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala  
 625 630 635 640

Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg  
 645 650 655

Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile  
 660 665 670

Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys  
 675 680 685

Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly

690		695		700
Arg Arg Arg Tyr Val	Pro Asp Leu Asn Ala	Arg Val Lys Ser Val	Arg	
705	710	715	720	
Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala				
	725	730	735	
Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg				
	740	745	750	
Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu				
	755	760	765	
Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu				
	770	775	780	
Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val				
	785	790	795	800
Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly				
	805	810		

<210> 587

<211> 2433

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 587

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caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagagaaga cggggatgtg	180
gtgatcgtgg tctttgacgc caaggccccc tccttcgcgc acgaggccta cgggggggtac	240
aaggcggggc gggccccgac ccccgaggac ttcccccggc agctcgccct catcaaggag	300
ctggtggacc tcctggggct ggcgcgcctc gaggtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaaaag gagggctacg aggtgcgcat tctcaccggc	420
gaccgcgacc tttaaccaact cgtctccgac cgcgtcgcca ggccggagca gtgggtggac	480



taccgggcct	tggccgggga	cccttccgac	aacatccccg	gcgtgaaggg	catcggggag	540
aagacggcga	ggaagcttct	ggaggagtgg	gggagcgtgg	aagccctcct	caagaacctg	600
gaccggctga	agcccgccat	ccgggagaag	atcctggccc	acatggagga	cctcaagcta	660
tccctggagc	tatcccggtt	gcgcaccgac	ctccccctgg	aggtggacct	cgcccagggg	720
cgggagcccc	accgggaggg	gcttaaggcc	tttttggaga	ggctggagtt	cggaagcctc	780
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ctaaaggacc	tcaaggaggt	ccggggcctc	ctcgccaagg	acctcgccgt	cttggcctcg	1020
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ccttcgaaca	ccacccccga	gggggtggcg	cggcgctacg	ggggggagtg	gacggaggac	1140
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ctacgggagg	cccaccccat	cgtggagaag	atcctccagc	accgggagct	caccaagctc	1560
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caggtcgcca	acgagctcct	cctggaggcc	ccccaaagcg	gggccgagga	ggtggcggct	2340

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 gggatggggg aggactggct ttccgccaag ggt 2433

<210> 588

<211> 811

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 588

Met Glu Phe Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val  
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Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu  
 20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys  
 35 40 45

Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val  
 50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr  
 65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
 85 90 95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val  
 100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala  
 115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Gly Asp Arg Asp Leu  
 130 135 140

Tyr Gln Leu Val Ser Asp Arg Val Ala Arg Pro Glu Gln Trp Val Asp  
 145 150 155 160

Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile Pro Gly Val Lys

165								170				175			
Gly	Ile	Gly	Glu 180	Lys	Thr	Ala	Arg	Lys 185	Leu	Leu	Glu	Glu	Trp 190	Gly	Ser
Val	Glu	Ala 195	Leu	Leu	Lys	Asn	Leu 200	Asp	Arg	Leu	Lys	Pro 205	Ala	Ile	Arg
Glu	Lys 210	Ile	Leu	Ala	His	Met 215	Glu	Asp	Leu	Lys	Leu 220	Ser	Leu	Glu	Leu
Ser 225	Arg	Val	Arg	Thr	Asp 230	Leu	Pro	Leu	Glu	Val 235	Asp	Leu	Ala	Gln	Gly 240
Arg	Glu	Pro	Asp	Arg 245	Glu	Gly	Leu	Lys	Ala 250	Phe	Leu	Glu	Arg	Leu 255	Glu
Phe	Gly	Ser	Leu 260	Leu	His	Glu	Phe	Gly 265	Leu	Leu	Glu	Ser	Pro 270	Val	Ala
Ala	Glu	Glu 275	Ala	Pro	Trp	Pro	Pro 280	Pro	Glu	Gly	Ala	Phe 285	Val	Gly	Tyr
Val 290	Leu	Ser	Arg	Pro	Glu	Pro 295	Met	Trp	Ala	Glu	Leu 300	Asn	Ala	Leu	Ala
Ala 305	Ala	Trp	Gly	Gly	Arg 310	Val	His	Arg	Ala	Ala 315	Asp	Pro	Leu	Ala	Gly 320
Leu	Lys	Asp	Leu	Lys 325	Glu	Val	Arg	Gly	Leu 330	Leu	Ala	Lys	Asp	Leu 335	Ala
Val	Leu	Ala	Ser 340	Arg	Glu	Gly	Leu	Asp 345	Leu	Val	Pro	Gly	Asp 350	Asp	Pro
Met	Leu	Leu 355	Ala	Tyr	Leu	Leu	Asp 360	Pro	Ser	Asn	Thr	Thr 365	Pro	Glu	Gly
Val 370	Ala	Arg	Arg	Tyr	Gly	Gly 375	Glu	Trp	Thr	Glu	Asp 380	Ala	Ala	His	Arg
Ala 385	Leu	Leu	Ser	Glu	Arg 390	Leu	His	Arg	Asn	Leu 395	Leu	Lys	Arg	Leu	Glu 400
Gly	Glu	Glu	Lys	Leu 405	Leu	Trp	Leu	Tyr	His 410	Glu	Val	Glu	Lys	Pro 415	Leu

Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val  
 420 425 430

Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg  
 435 440 445

Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn  
 450 455 460

Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro  
 465 470 475 480

Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala  
 485 490 495

Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu  
 500 505 510

Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu  
 515 520 525

Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn  
 530 535 540

Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu  
 545 550 555 560

Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala  
 565 570 575

Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln  
 580 585 590

Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile  
 595 600 605

Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp  
 610 615 620

Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala  
 625 630 635 640

Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg  
 645 650 655

Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile  
 660 665 670

Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys  
675 680 685

Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly  
690 695 700

Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg  
705 710 715 720

Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala  
725 730 735

Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg  
740 745 750

Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu  
755 760 765

Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu  
770 775 780

Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val  
785 790 795 800

Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly  
805 810

<210> 589

<211> 2493

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 589

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cagatggtct acggcttcgc ccggagcctc ctcaaggccc tcaaggagga cggggacgcg	180
gtgatcgtgg tctttgacgc cgaggccccc tccttcgcgc accagacctt cgaggcctac	240
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ctcgccaccc	tggccaagaa	ggcggaaaag	gagggctacg	aggtgcgcat	cctcaccgcg	420
gaccgggacc	tttaccagct	tctttccgac	cgcattcacg	tccttcaccc	cgaggggtac	480
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cttgccatcc	cctacgagga	ggcgtggccc	tttatagagc	gctacttcca	aagcttcccc	2100
aaggtgcggg	cctggataga	aaagaccctg	gaggagggga	ggaagcgggg	ctacgtggaa	2160

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gaggccgcgg agcgcatggc cttcaacatg cccgtccagg gcaccgccgc cgacctcatg 2280  
aagctcgcca tggatgaagct cttccccgcg ctccgggaga tgggggcccg catgctcctc 2340  
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gggatggggg aggactggct ttccgccaag ggt 2493

<210> 590

<211> 831

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 590

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val  
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Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu  
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe Ala Arg  
35 40 45

Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val  
50 55 60

Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr  
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
85 90 95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val  
100 105 110

Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala  
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu

130		135		140											
Tyr 145	Gln	Leu	Leu	Ser	Asp 150	Arg	Ile	His	Val	Leu 155	His	Pro	Glu	Gly	Tyr 160
Leu	Ile	Thr	Pro	Ala 165	Trp	Leu	Trp	Glu	Lys 170	Tyr	Gly	Leu	Arg	Pro	Asp 175
Gln	Trp	Ala	Asp 180	Tyr	Arg	Ala	Leu	Thr 185	Gly	Asp	Glu	Ser	Asp 190	Asn	Leu
Ser	Gly	Val 195	Lys	Gly	Ile	Gly	Glu 200	Lys	Thr	Ala	Arg	Lys 205	Leu	Leu	Glu
Glu	Trp	Gly 210	Ser	Leu	Glu	Ala 215	Leu	Leu	Lys	Asn	Leu	Asp 220	Arg	Leu	Lys
Pro 225	Ala	Ile	Arg	Glu	Lys 230	Ile	Leu	Ala	His	Met 235	Asp	Asp	Leu	Lys	Leu 240
Ser	Leu	Glu	Leu	Ser 245	Arg	Val	Arg	Thr	Asp 250	Leu	Pro	Leu	Glu	Val 255	Asp
Phe	Ala	Lys	Arg 260	Arg	Glu	Pro	Asp	Arg 265	Glu	Arg	Leu	Arg	Ala	Phe	Leu
Glu	Arg	Leu 275	Glu	Phe	Gly	Ser	Leu 280	Leu	His	Glu	Phe	Gly 285	Pro	Leu	Glu
Ser	Pro 290	Arg	Ala	Ala	Glu	Glu 295	Ala	Pro	Trp	Pro	Pro 300	Pro	Glu	Gly	Ala
Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu 320
305					310					315					
Asn	Ala	Leu	Ala	Ala 325	Ala	Arg	Gly	Gly	Arg 330	Val	His	Arg	Ala	Ala 335	Asp
Pro	Leu	Ala	Gly 340	Leu	Lys	Asp	Leu	Lys 345	Glu	Val	Arg	Gly	Leu	Leu	Ala
Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	Leu	Asp 365	Leu	Val	Pro
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Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp 380	Pro	Ser	Asn	Thr
370							375								



Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp  
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Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu  
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Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val  
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Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val  
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Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu  
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Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro  
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Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu  
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Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser  
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Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val  
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Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr  
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Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His  
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Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser  
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Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg  
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Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu  
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Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp  
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Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln  
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Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu  
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Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met  
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Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala  
675 680 685

Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala  
690 695 700

Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu  
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Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val  
725 730 735

Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val  
740 745 750

Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe  
755 760 765

Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn  
770 775 780

Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala  
785 790 795 800

Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu  
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21

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28

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26

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26

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15

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21

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29

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24

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16

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19

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18

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16

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28

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gggccagagg gctgattag 19

<210> 723

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 723

aggcagtcag agaggcg 17

<210> 724

<211> 28

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14

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<400> 726

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25

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<210> 732  
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<400> 732  
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 27

<210> 733  
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<400> 734  
aggcagtcag agtgatc 17

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14

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24

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25

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<400> 739

cctgggccag agggctgatt

20

<210> 740

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<400> 740

cagtcagatc agtgatc

17

<210> 741

<211> 28

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cggaagaagc agttggtgat ctcggcgg

28

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<222> (4)..(4)

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<210> 745

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<400> 745  
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<210> 746

<211> 23

<212> DNA  
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<223> Synthetic

<400> 746  
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23

<210> 747

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27

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<400> 748  
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11

<210> 749

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 ccgccgagat cactctgatg cctggg 26  
  
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20

<210> 757  
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<400> 757  
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28

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<210> 759

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ccgtcacgcc tccatctggt taggg 25

<210> 760

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<400> 760

caggtcctgg aaggagcact ta 22

<210> 761

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<400> 761

ccatcagctt ctttgttctt gtcac 26

<210> 762

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<223> Synthetic

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gccctaaaca gatggaggcg

20

<210> 763

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14

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26

<210> 766

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<400> 766

caggtcctgg aaggagcact ta

22

<210> 767

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26

<210> 768

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22

<210> 773  
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27

<210> 774  
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28

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 23

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 22

<210> 778  
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 cggaagaagc agttggaggc gtgacggt 28  
  
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26

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